

FIGURE 1A

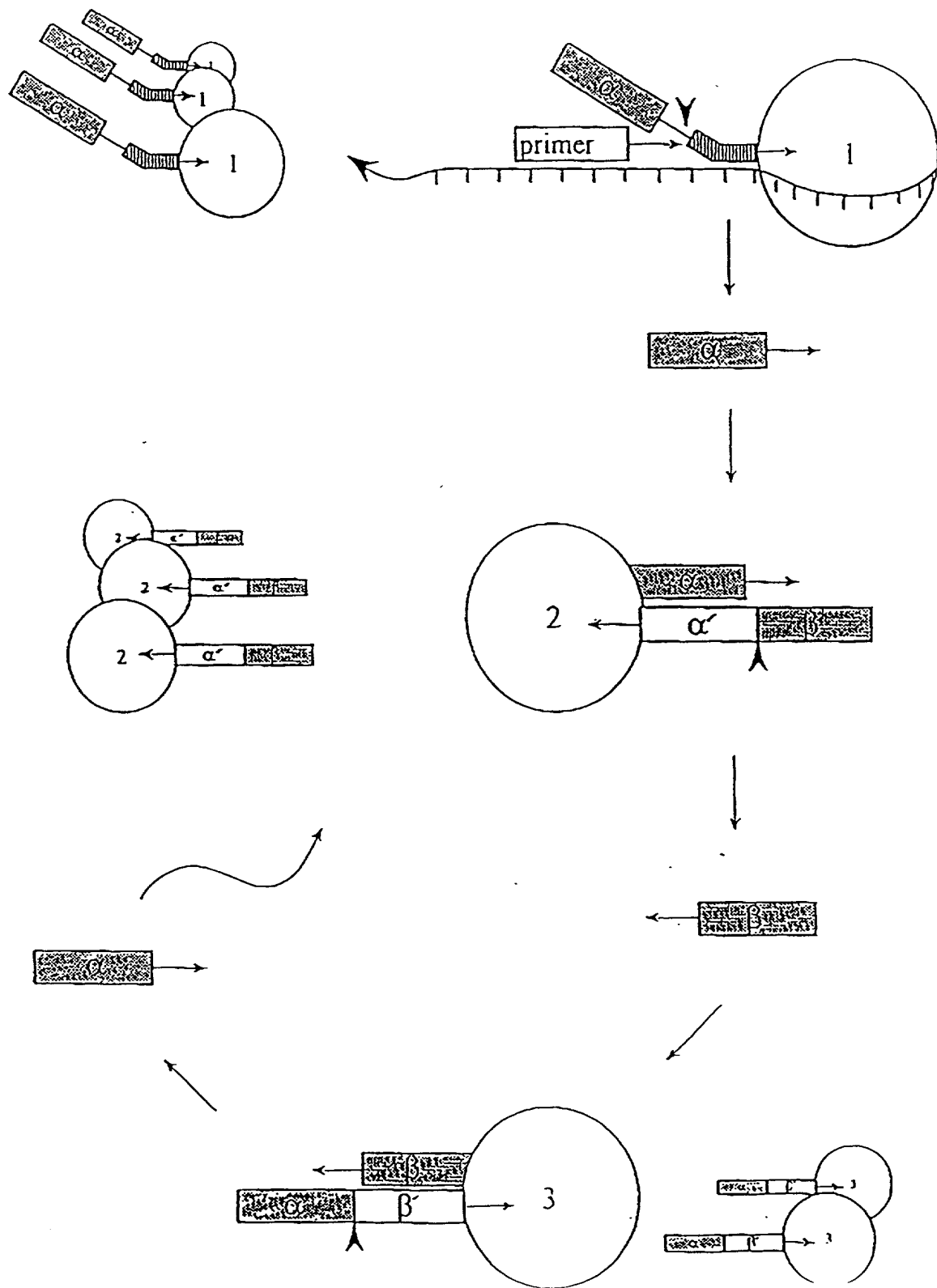
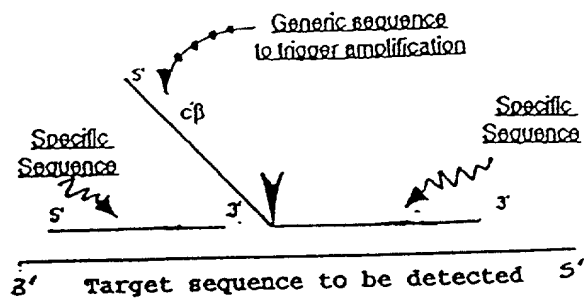
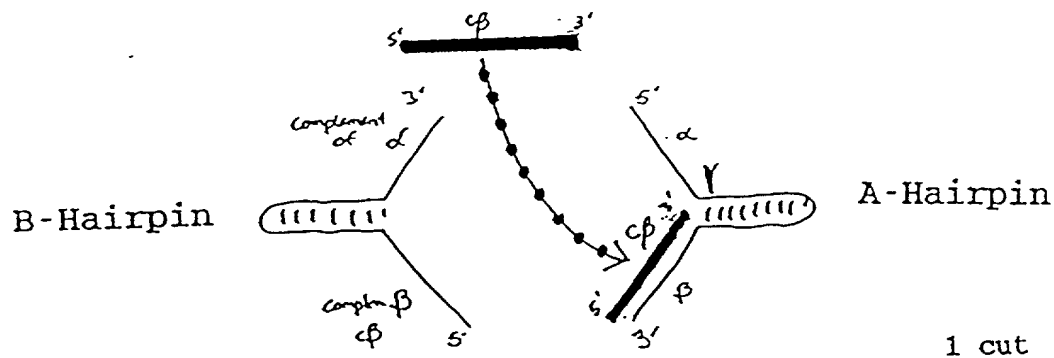


FIGURE 1 B

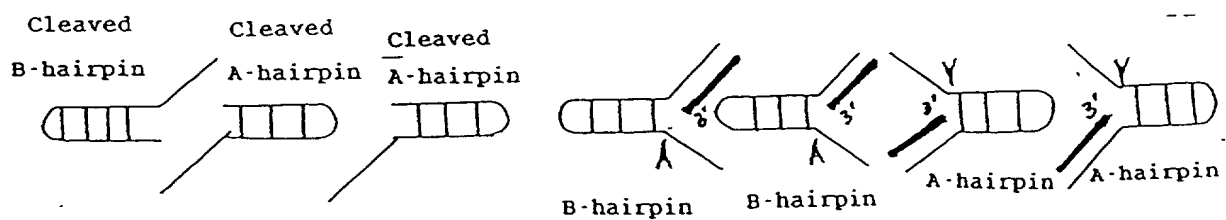
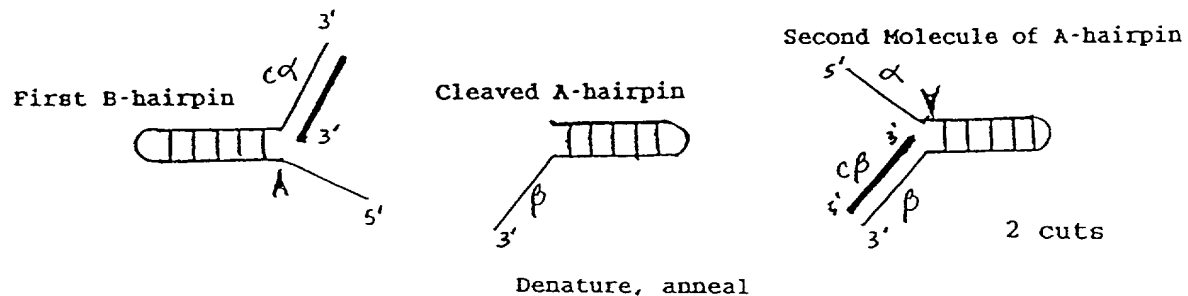
PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION



Denature, anneal



4 cuts









FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCGCGCGCGCTCGAGGAGGAGGTCTTCGCGCTGCGCGCGCGCGCTTCAACCTCAACTCGCGCGGAG	1464
DNAPTAA (SEQ ID NO:1)	.....GG.....CG.....	1461
DNAPTTL (SEQ ID NO:2)	.....G.G.....AG.G.....	1470
DNAPTTH (SEQ ID NO:3)	.....T.....G.....	
MAJORITY	CAGCTGGAAAGGCTGCTCTTTGACGAGCTXGCGCTTCGCGCGCTCGGCAAGACGGAGAAACXGGCAAGC	1534
DNAPTAA	.....C.....A.....	1531
DNAPTTL	.....GC.....G.C.G.T.....	1540
DNAPTTH	.....TA.....T.G.G.....	
MAJORITY	GCTCCAGCAGCGCGCGCTGCTGGAGGCGCTXGCGAGCGCGCGCGCTCGTGAGAAAGATCCTGCAGTA	1604
DNAPTAA	.....C.....C.....	1601
DNAPTTL	.....T.....G.A.....CGGC.....	1610
DNAPTTH	.....G.....A.G.....	
MAJORITY	CGCGGAGCTCAGCAAGCTCAAGAACACCTACATXGACCGCGCTGCCXGXCTCGTCCACCGCGAGGACGGCG	1674
DNAPTAA	.....G.....G.....T.....G.A.....	1671
DNAPTTL	.....A.....A.....G.C.....	1680
DNAPTTH	.....G.C.....G.AAG.....	
MAJORITY	CGCGCTCCACACCGCTTCAAGCAGACGGCGCACCGCGCGCGCTTAGTAGCTCCGACCGCGCAAGCTGC	1744
DNAPTAA	.....A.....T.....	1741
DNAPTTL	.....C.....TGC.....	1750
DNAPTTH	.....G.....	

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	AGAACATCCCGTCCGACCCGCTGGGCCAGAGGATCCGCCGGGGCTTCGTGCCCGAGGAGGGXTGGGT	
DNAPTAQ	(SEQ ID NO:1)	.....G..T..G.....A..C.....G...C..	1814
DNAPTFL	(SEQ ID NO:2)	.....G.....T.....A.....C.....C.....	1811
DNAPTHH	(SEQ ID NO:3)	.....CT.....C.....T.....C.....C.....	1820
MAJORITY		GTTGGTGGCGCTAGCCAGATAGAGCTCCGGGTCTGGCCGACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ		A.....T.T.....C.....A.....G.....C.....	1884
DNAPTFL		.....T.T.....C.....T.....T.....A.....	1881
DNAPTHH		.....T.T.....C.....C.....C.....A.....	1890
MAJORITY		ATCCGGGTCTTCAGAGGGAGGACATCCACAGCCGACGCGGCTGGATGTTCCGGCGTCCCGCCGG	
DNAPTAQ		.....C.....C.....GG.....G.....G.....	1954
DNAPTFL		.....T.....T.....A.....A.....TT.....C..	1951
DNAPTHH		.....A.....A.....A.....A.....	1960
MAJORITY		AGCGCGTGGACCCCTGATCGCGCGGGGGCCAGACCATCAACTTCGGGGTCTCTACGGCATGTCCGG	
DNAPTAQ		.....A..G..A.....T.....GG..G.....G.....	2024
DNAPTFL		.....A..G..A.....T.....GG..G.....G.....	2021
DNAPTHH		.....A..G..A.....T.....GG..G.....G.....	2030
MAJORITY		CCACCGCCTCTCCAGGAGCTTGGCATCCGCTACGAGAGGGGGTGGCCTTCATTGAGCGGTACTTCCAG	
DNAPTAQ		.....A.....A.....T.....CCA.....T...	2094
DNAPTFL		.....GG.....T.....T.....T.....A.....	2091
DNAPTHH		.....TA..G.....T.....A.....A.....	2100



FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCGCCAAGGTCCGGGGCCTGGATTGAGAAACCCCTGGAGGAGGGGAGGGGGGTACGTGGAGA	2164
DNAPTAG (SEQ ID NO:1)	.....	2161
DNAPTL (SEQ ID NO:2)	.....	2170
DNAPTH (SEQ ID NO:3)	.....	
MAJORITY	CCCTCTTCGGGGCGCGGGCTAGCTGCCCGACCTCAAGCGCGGGGTGAAGAGCGTGGGGAGGGGGCGGA	2234
DNAPTAG	.....	2231
DNAPTL	.....	2240
DNAPTH	.....	
MAJORITY	GGGCATGGCCCTTCAACATGCCCGTCCAGGGGACCGCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC	2304
DNAPTAG	.....	2301
DNAPTL	.....	2310
DNAPTH	.....	
MAJORITY	TTCCCGCGGCTXCAGGAAATGGGGGCGAGGATGCTCCTXCAGGTCGACGAGGAGCTGCTCCTCGAGGGCGC	2374
DNAPTAG	.....	2371
DNAPTL	.....	2380
DNAPTH	.....	
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCGGCTTGGCCAAAGGAGGTCATGGAGGGGGTGTATCCCGTGGCGGT	2444
DNAPTAG	.....	2441
DNAPTL	.....	2450
DNAPTH	.....	

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGCCCTGGAGGTGGAGGTGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG
DNAPTAA	(SEQ ID NO:1)	.....A.....GA
DNAPTFL	(SEQ ID NO:2)	.....CC.....GT...
DNAPTHH	(SEQ ID NO:3)	.....T.....GT...

2499  
2496  
2505

FIGURE 3

MAJORITY (SEQ ID NO:8)	MXA M L P L F E P K G R V L L V D G H L A Y R T F F A L K G L T T S R G E P V O A V Y G F A K S L L K A L K E D G . D A V X V V F D A K	
TAQ PRO (SEQ ID NO:4)	..... H . . . . .	69
TR PRO (SEQ ID NO:5)	..... V . V . . . .	68
TTH PRO (SEQ ID NO:6)	..... Y K . . F . . . .	70
MAJORITY	AP S F R H E A Y E A Y K A G R A P T P E D F P R O L A L I K E L V D L L G L X R L E V P G Y E A D D V L A T L A K K A E K E G Y E V R I L	
TAQ PRO	..... A . . . . . S . . . . .	139
TR PRO	..... V . . . . . F . . . . . R . . . . .	138
TTH PRO	..... F T . . . . .	140
MAJORITY	T A D R D L Y Q L L S D R I A V L H P E G Y L I T P A W L W E K Y G L R P E Q W V D Y R A L X G D P S D N L P G V K G I G E K T A X K L L X	
TAQ PRO	..... H . . . . . D . . A . . . . . T . . E . . . . . R . . . . . E	209
TR PRO	..... E . . . . . Y . . . . . A . . . . . I . . . . . Q R . . I R	208
TTH PRO	..... V . . . . . H . . . . . F . . . . . V . . . . . L . . . . . K	210
MAJORITY	E W G S L E N L L K N L D R V K P . X X R E K I X A H M E D L X L S X X L S X V R T D L P L E V D F A X R R R E P D R E G L R A F L E R L E F	
TAQ PRO	..... L . . . . . A I . . . . . L . . . . . D . . K . . . . . W D . A K . . . . . K . . . . . R . . . . .	278
TR PRO	..... F Q H . . . . . S L . . . . . L Q . G . . . . . A . A . . . . . R K . . . . . Q . H . . . . . G R . . . . . T . N L . . . . .	277
TTH PRO	..... E N V . . . . . K . . . . . L . . . . . R . . . . . L E . . . . . R . . . . . L . . . . . Q G . . . . .	280
MAJORITY	G S L L H E F G L L E X P K A L E E A P W P P P E G A F V G F V L S R P E P M Y A E L L A L A A A R X G R V H R A X D P L X G L R D L K E V	
TAQ PRO	..... S . . . . . K . . . . . D . . . . . G . . . . . P E . Y K A . . . . . A	348
TR PRO	..... G . . . . . A . . . . . L . . S F . . . . . G . W E . . . . . L . . . . . Q . . . . . R . . . . . G .	347
TTH PRO	..... A . A P . . . . . K . . . . . C . D . . . . . A . . . . . A . . . . . K . . . . .	350

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKDLAVLALREGLDLXPGDDPHMLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)	.....S.....G.P.....E.....A.....A...WG	418
TR PRO (SEQ ID NO:5)	..I.....F.E.....A.....A.....QT.KE	417
TTH PRO (SEQ ID NO:6)	.....S.....V.....AH.....HR...LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PRO	.....R...R...A.....R.....A.....A.....	488
TR PRO	.....E.....R.....EA.V.Q.....	487
TTH PRO	.....K.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PRO	.....S.....S.....D.I.....	558
TR PRO	.....DR.....A.....K...	557
TTH PRO	.....R...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNQTATATGRLSSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDEHL	
TAQ PRO	.....L.....L.....	628
TR PRO	.....V...V.....	627
TTH PRO	.....A...A.....	630
MAJORITY	IRVFOEGRDIHTQTASWMFGVPPPEAVDPLMRRAAKTI NFGVLYGMSAHLRSOELAI PYEEAVAFIERYFQ	
TAQ PRO	.....E.....R.....Q.....	698
TR PRO	.....S...G.....G...S.....	697
TTH PRO	.....K.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRAWI EKTLEEGRRRGYVETLFGRRRYVPDLNARVKSUREAERMAFNMPVQGT AADLMKLAHVKL	768
TAQ PR0 (SEQ ID NO:4)	.....E.....	767
TR PR0 (SEQ ID NO:5)	Y.....G.....	770
TTT PR0 (SEQ ID NO:6)	.....K.....	
MAJORITY	FPRLEXMGARHMLQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PR0	.....E.....A.....R.....I.....	833
TR PR0	.....Q.....L.....D.....R.....W.....Q.....L.....	831
TTT PR0	.....R.....L.....QA.....E.....A.....KA.....M.....G.....	835

FIGURE 4

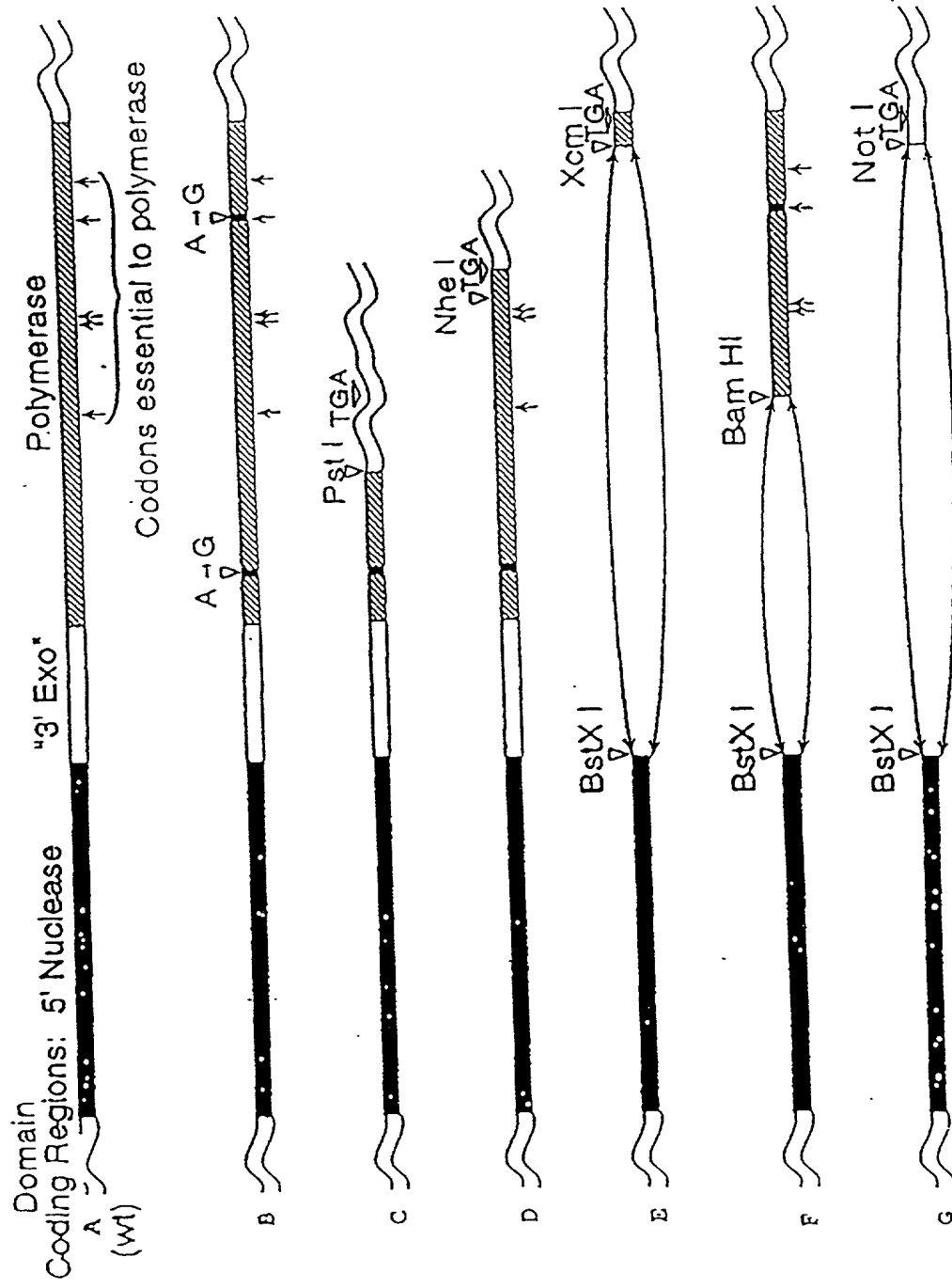


FIGURE 5

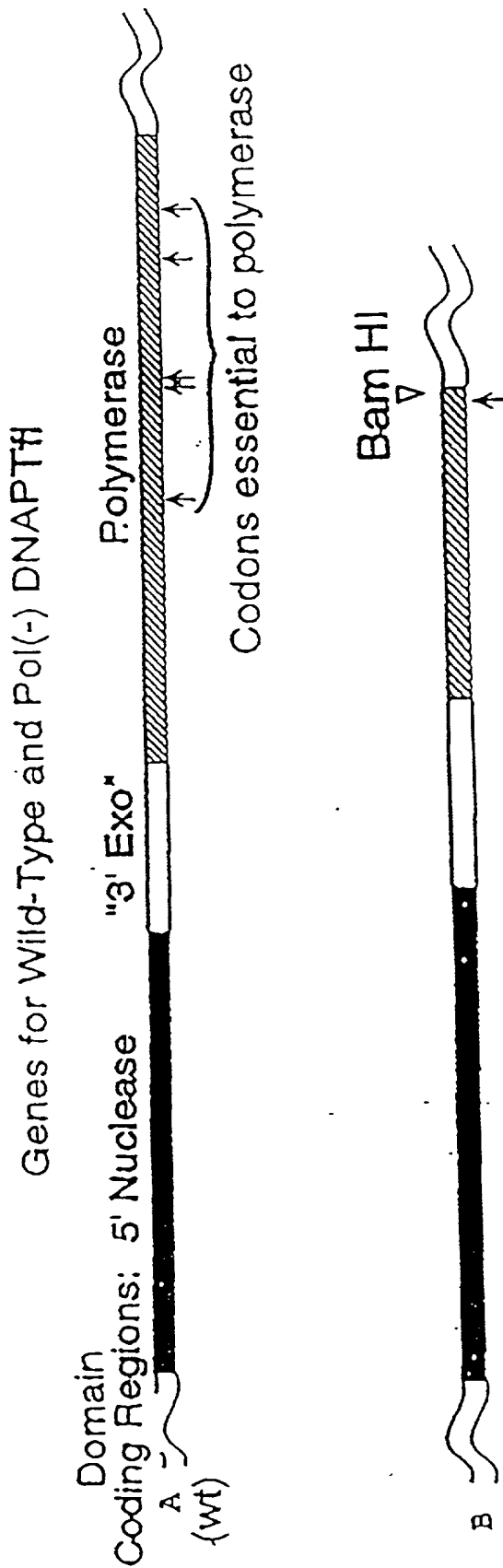
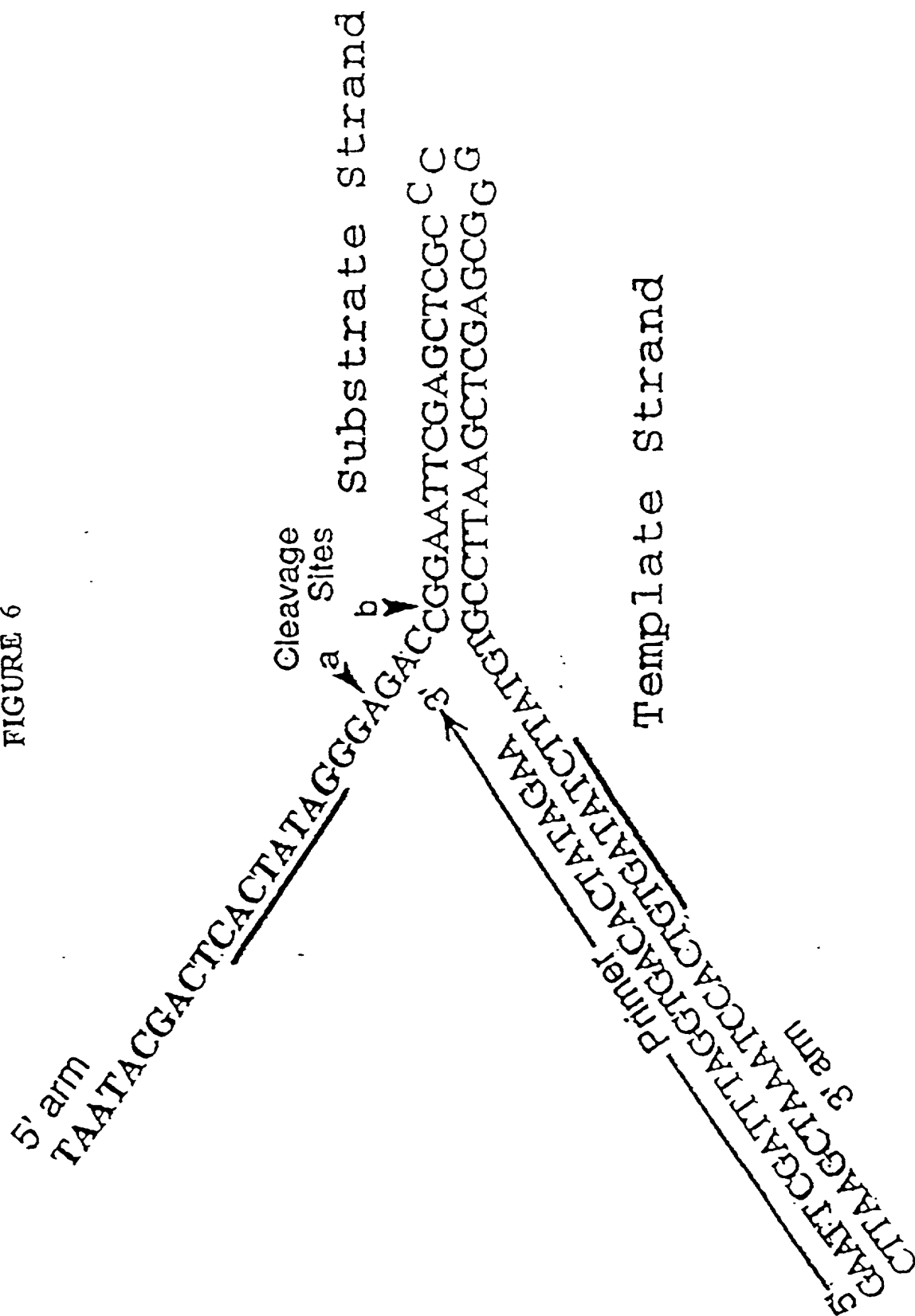


FIGURE 6





09340933 082901  
103230 52504650

FIGURE 7



T03230" 52504660

FIGURE 8

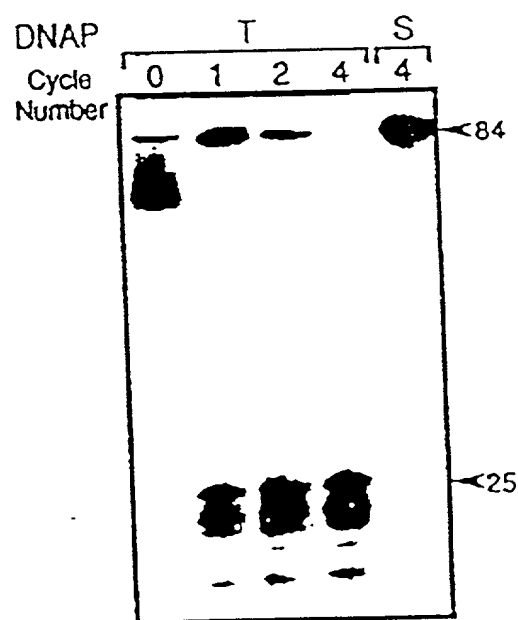


FIGURE 9

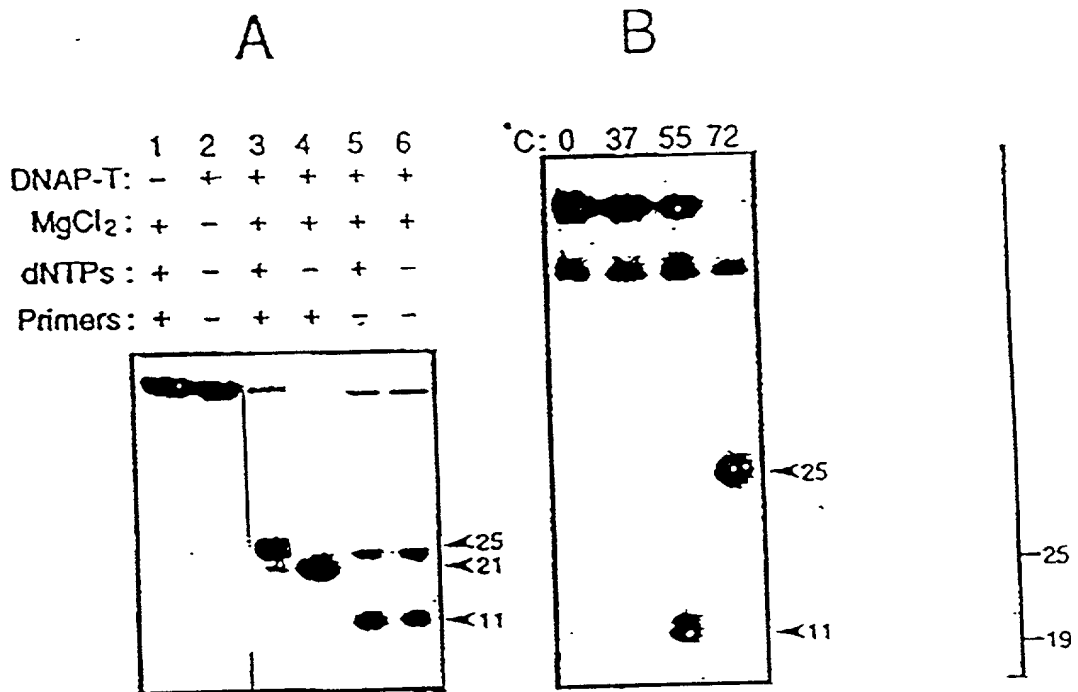


FIGURE 10

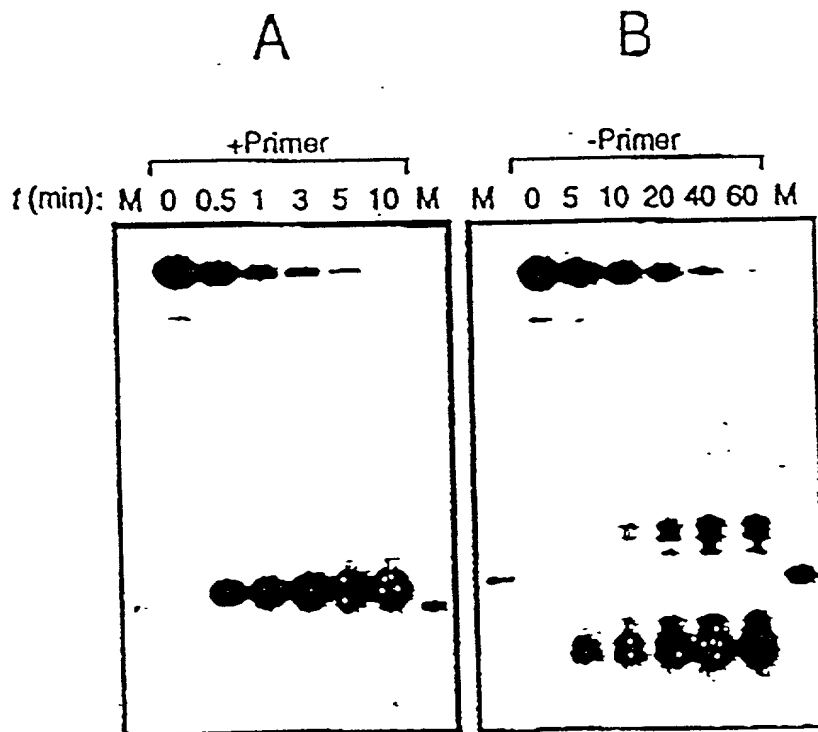




FIGURE 12

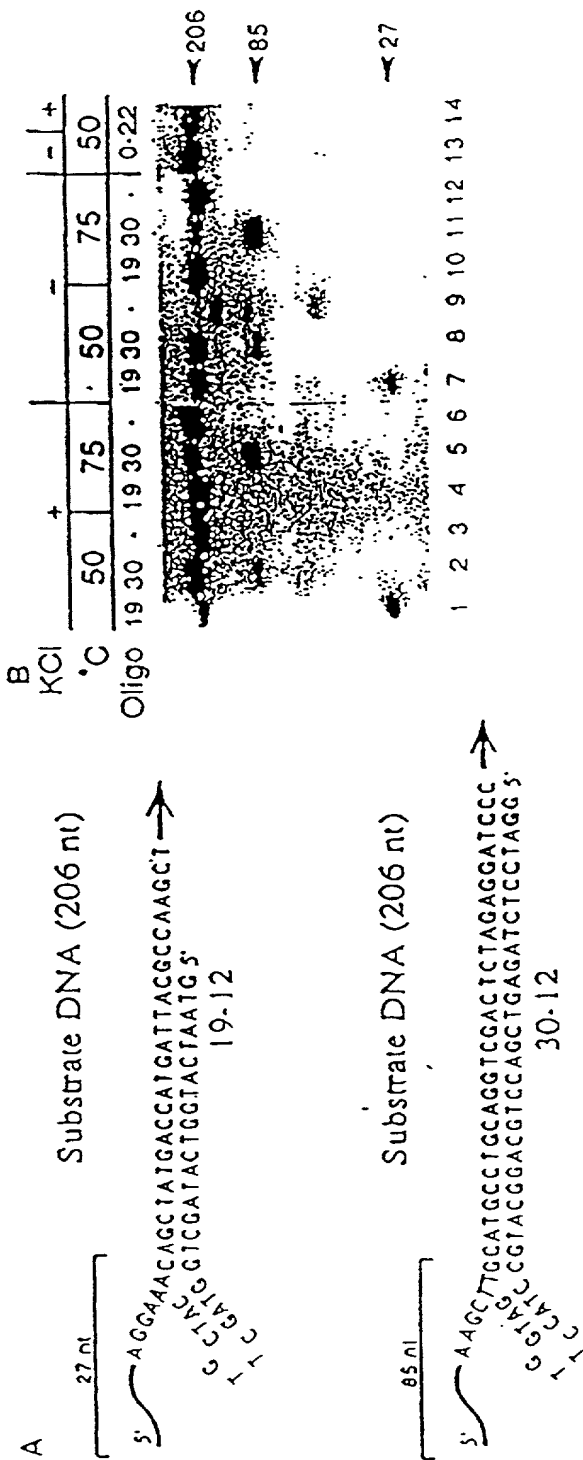


FIGURE 13

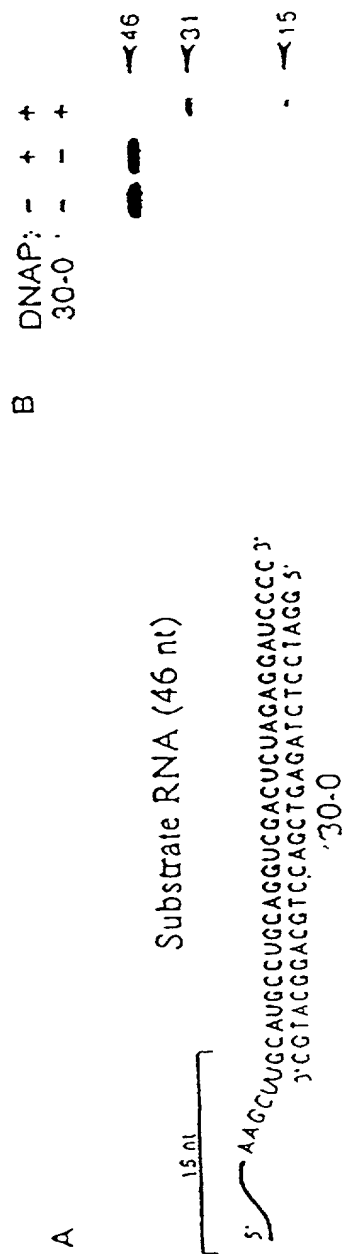
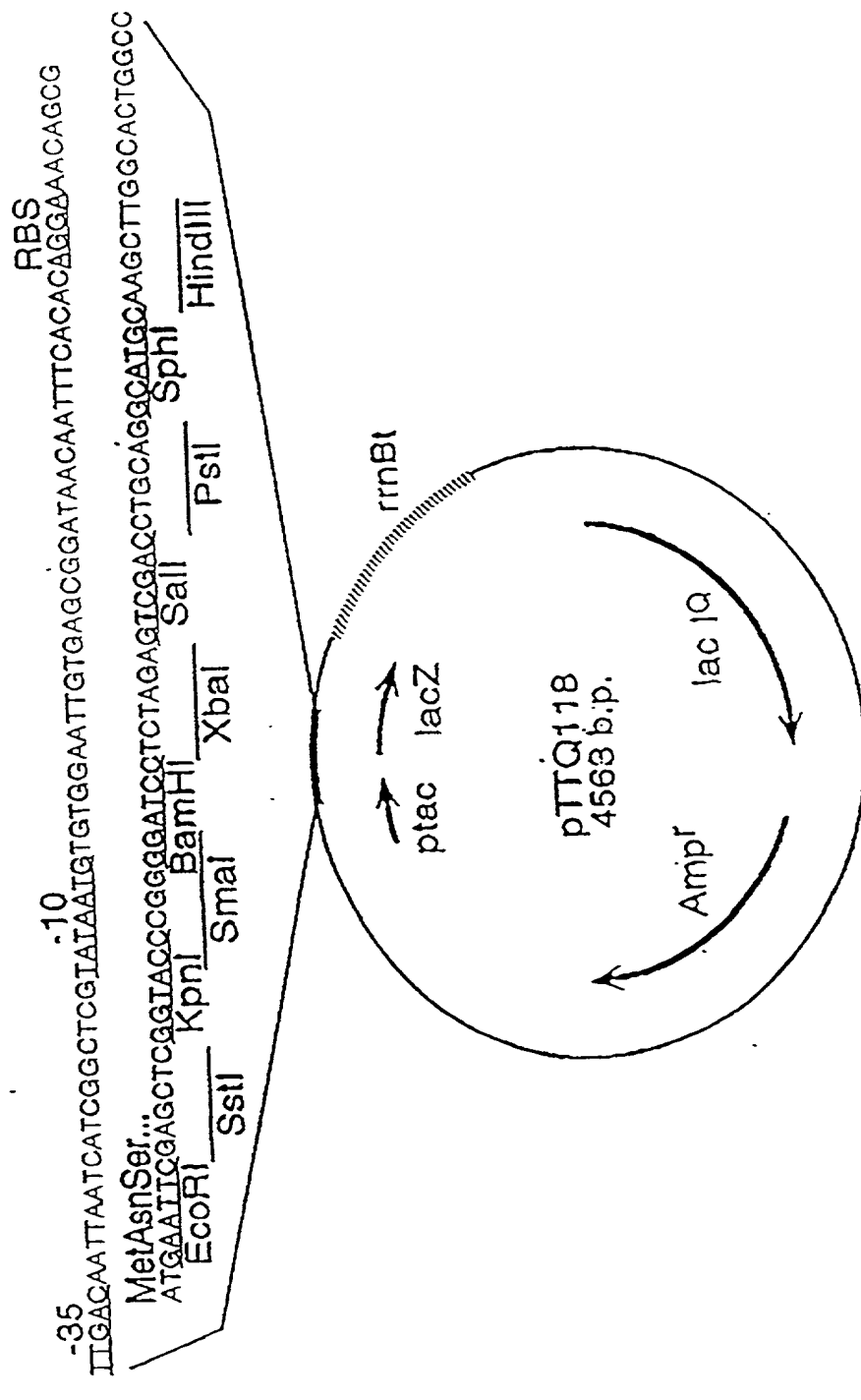


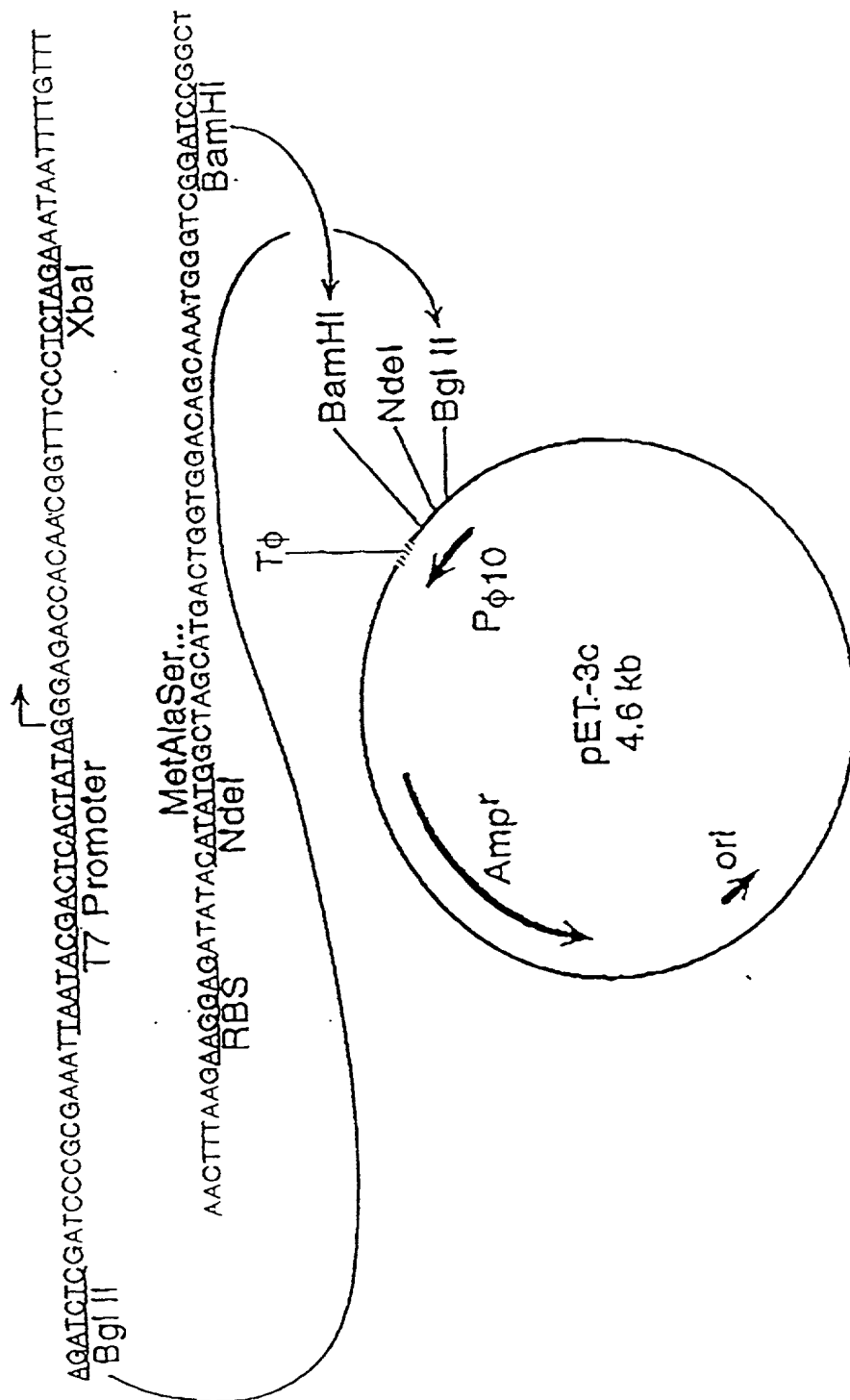
FIGURE 14



RBS: Ribosome binding site  
 ptac: Synthetic tac promoter  
 lacIQ: Lac repressor gene  
 lacZ: Beta-galactosidase alpha fragment  
 rrnBt: E. coli rrnB transcription terminator



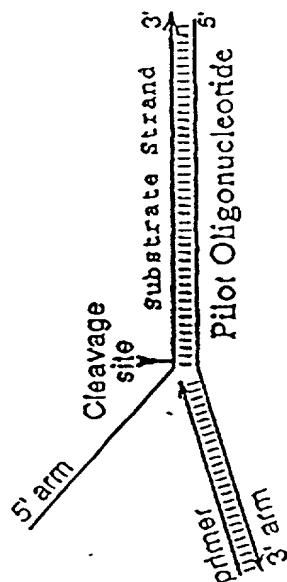
FIGURE 15



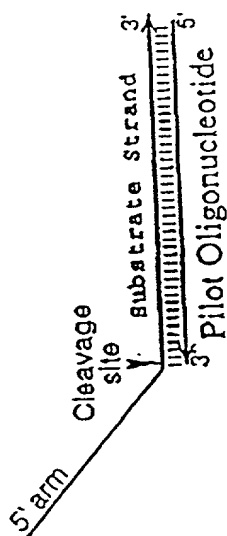
Pφ10: Bacteriophage T7 φ10 promoter  
 Tφ: T7 φ Terminator  
 RBS: Ribosome binding site

FIGURE 16

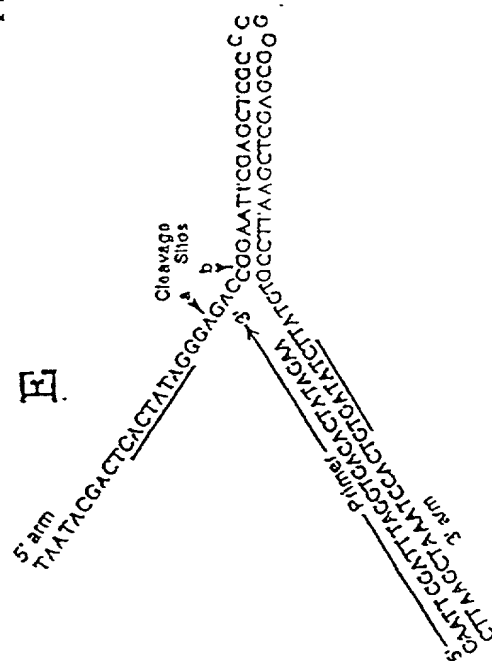
B



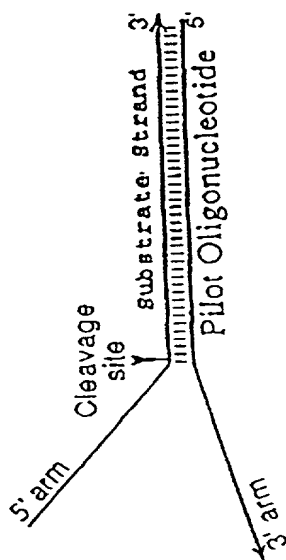
D



E



A



C

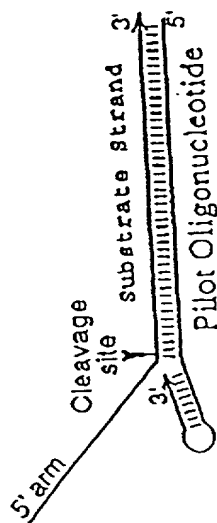


FIGURE 17

Uncleared substrate

Cleared substrate

dNTPs

Primer

Enzyme

FIGURE 18

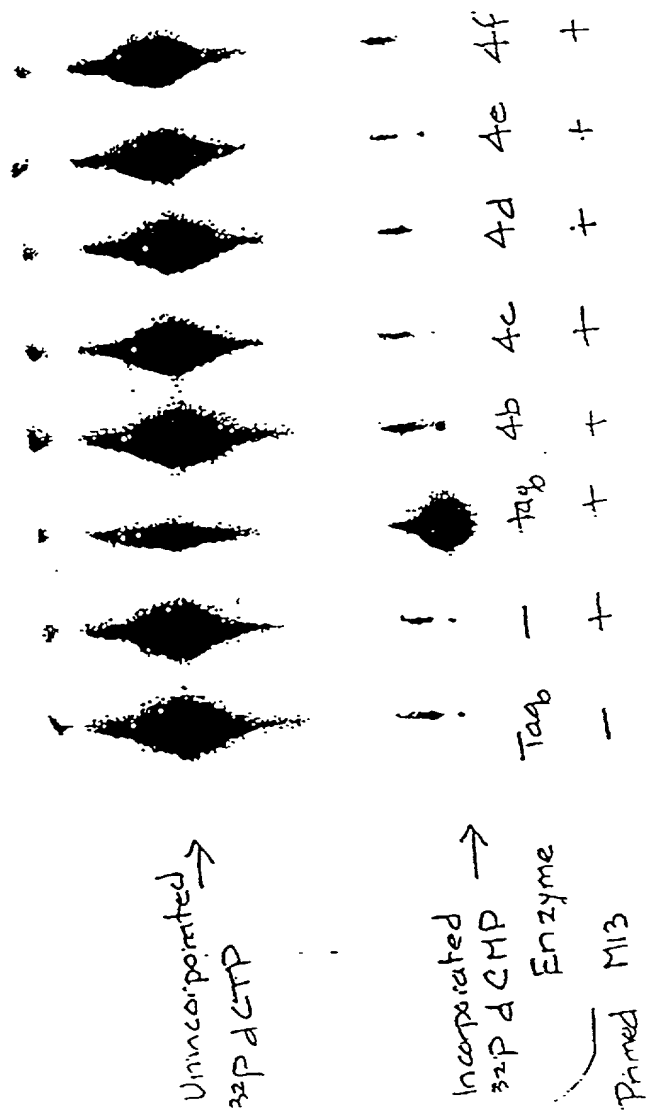
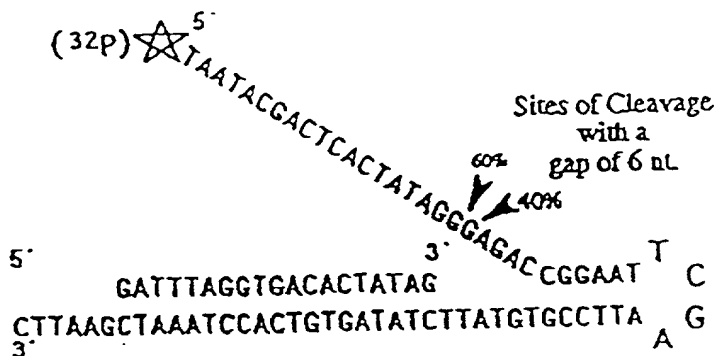


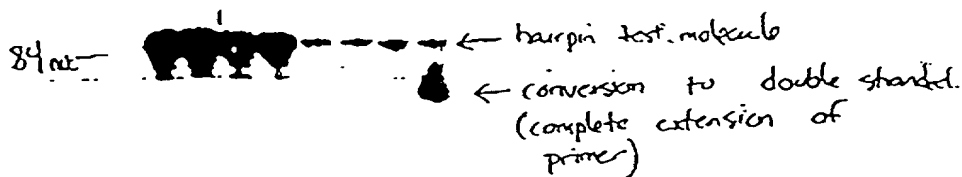
FIGURE 19

A



B

		4d		4b			
		No mutation		(2 pt. small activity)		Unmodified DNA Tag	
		Rel. Activity					
1	2	3	4	5	6	7	8
		C/A		T/A		T/A	
		+		+		+	



desired product  
 21 nuc.

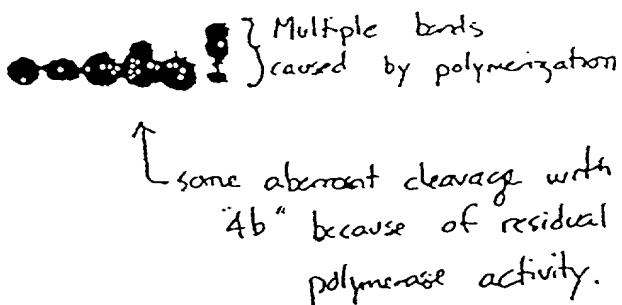
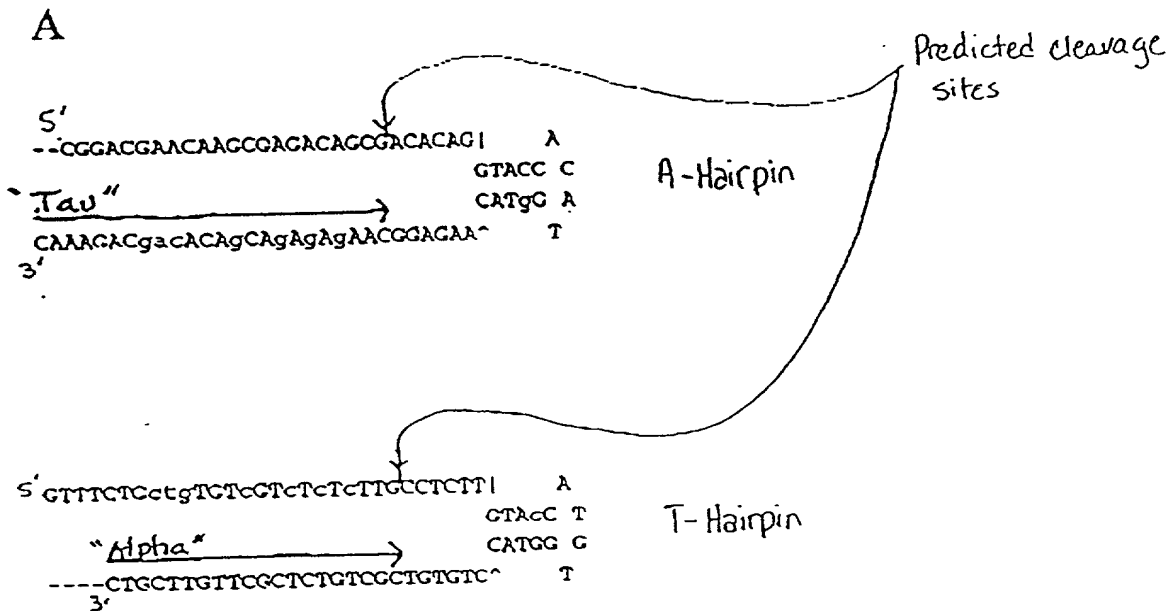
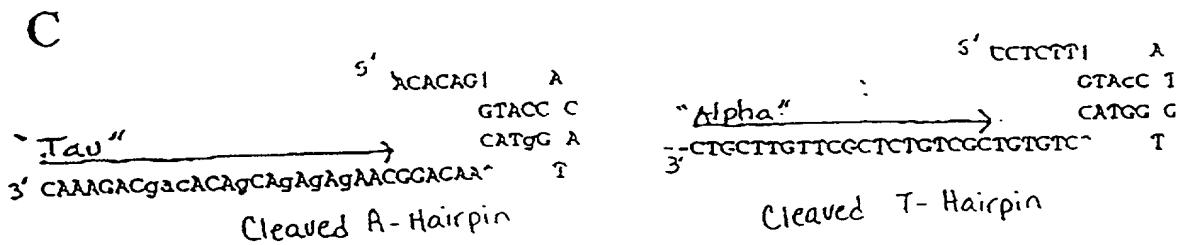


FIGURE 20



**B** Sequence of alpha primer:

5' GAC GAA CAA CCG AGA CAG CG 3'



**D**

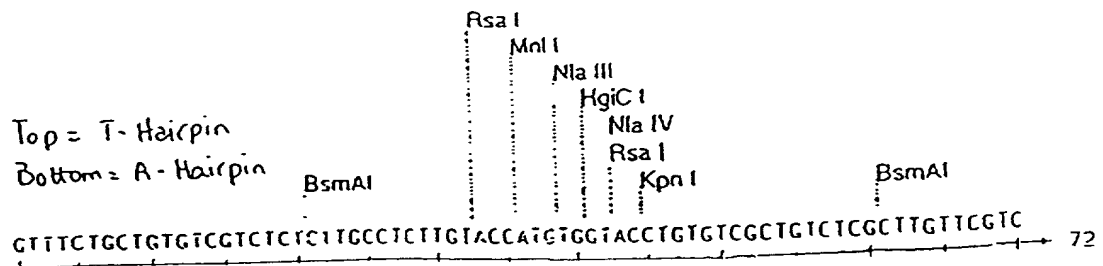


FIGURE 21

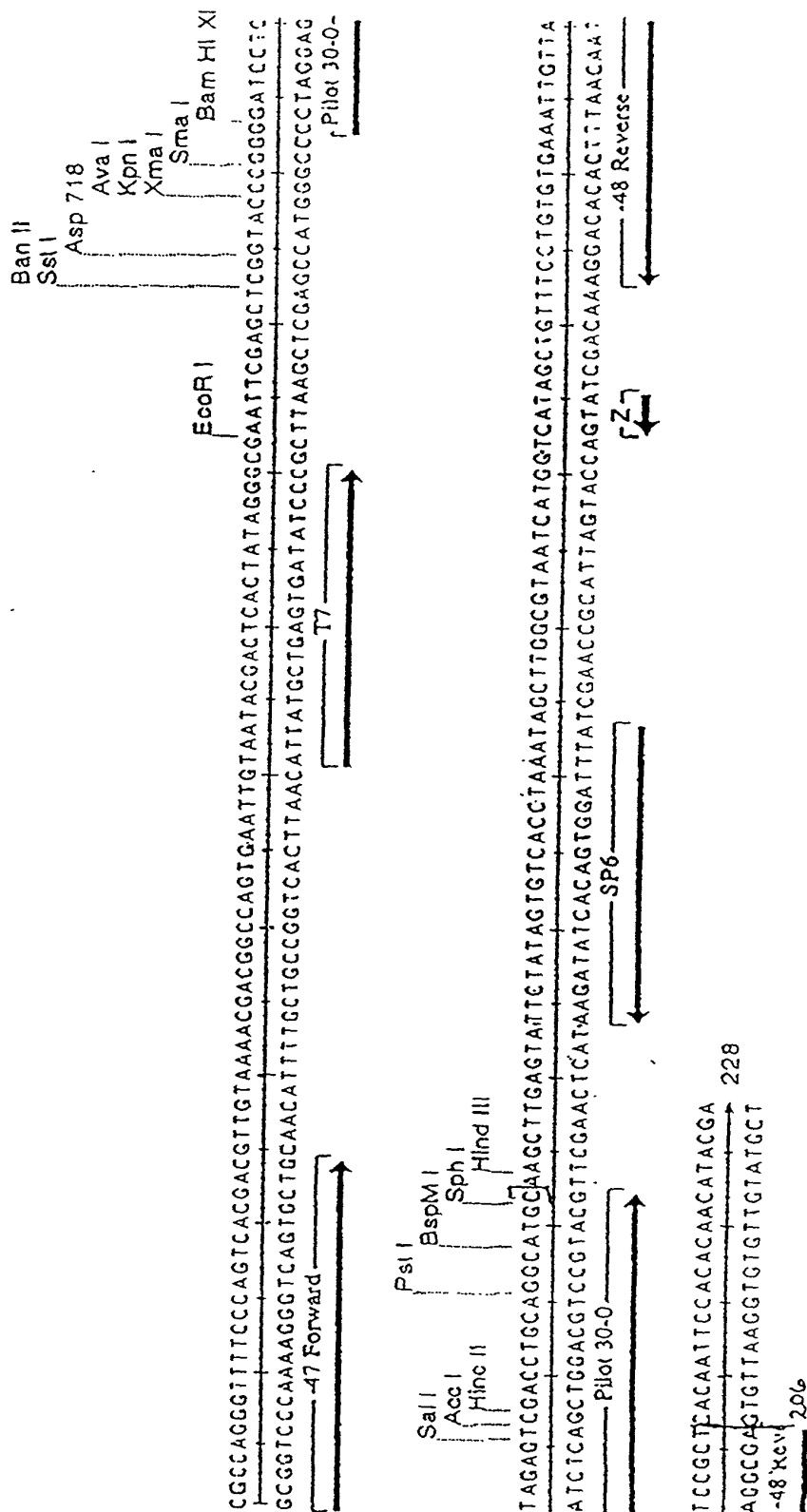


FIGURE 22A

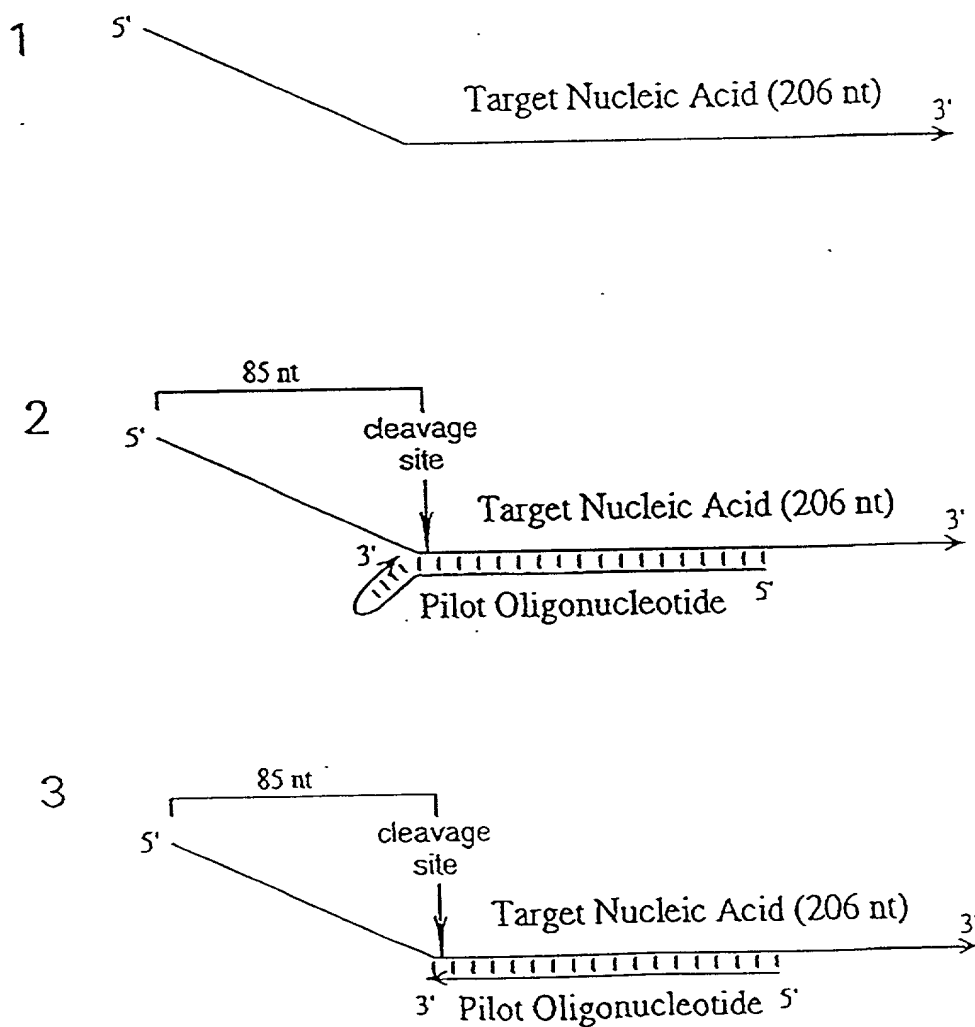




FIGURE 22B

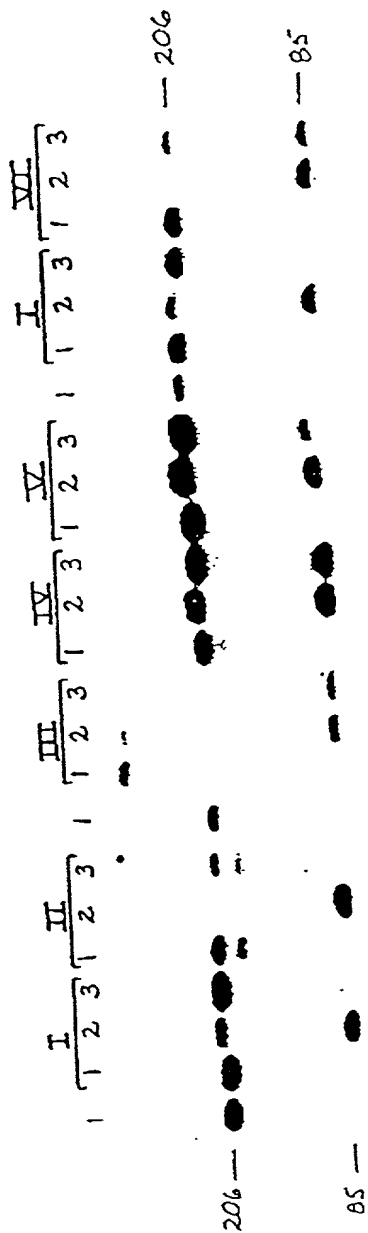


FIGURE 23

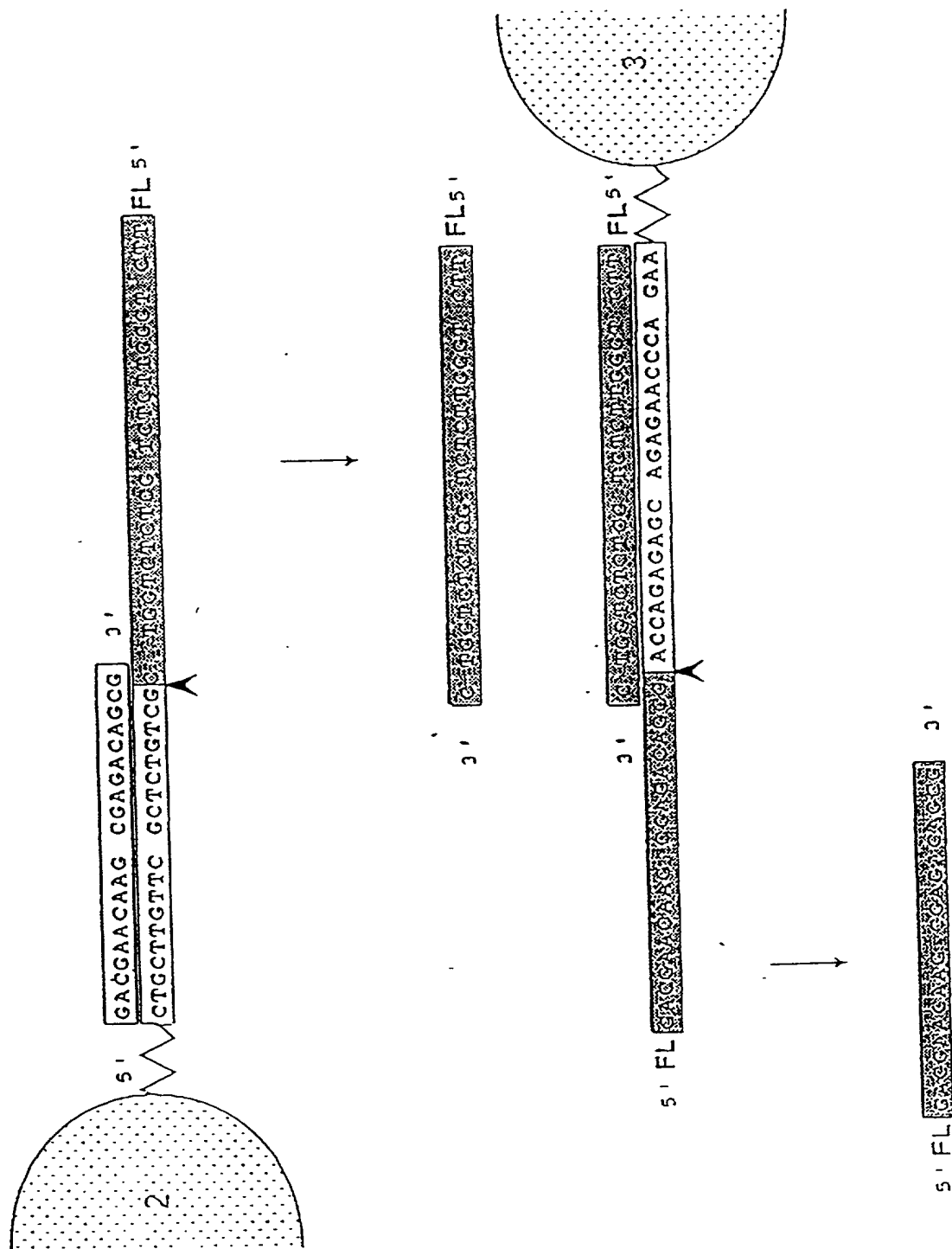
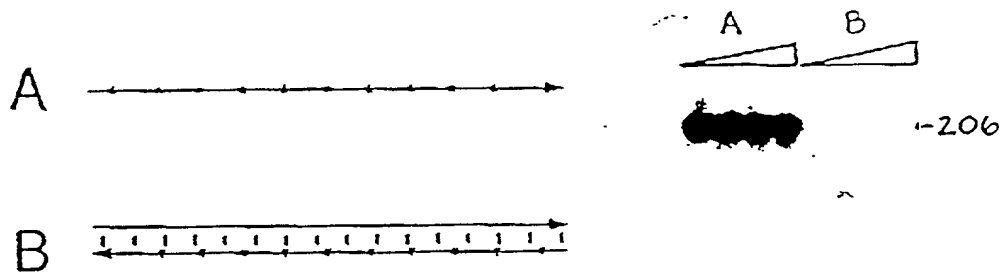






FIGURE 26



$\bullet = {}^{32}\text{P}$

FIGURE 27

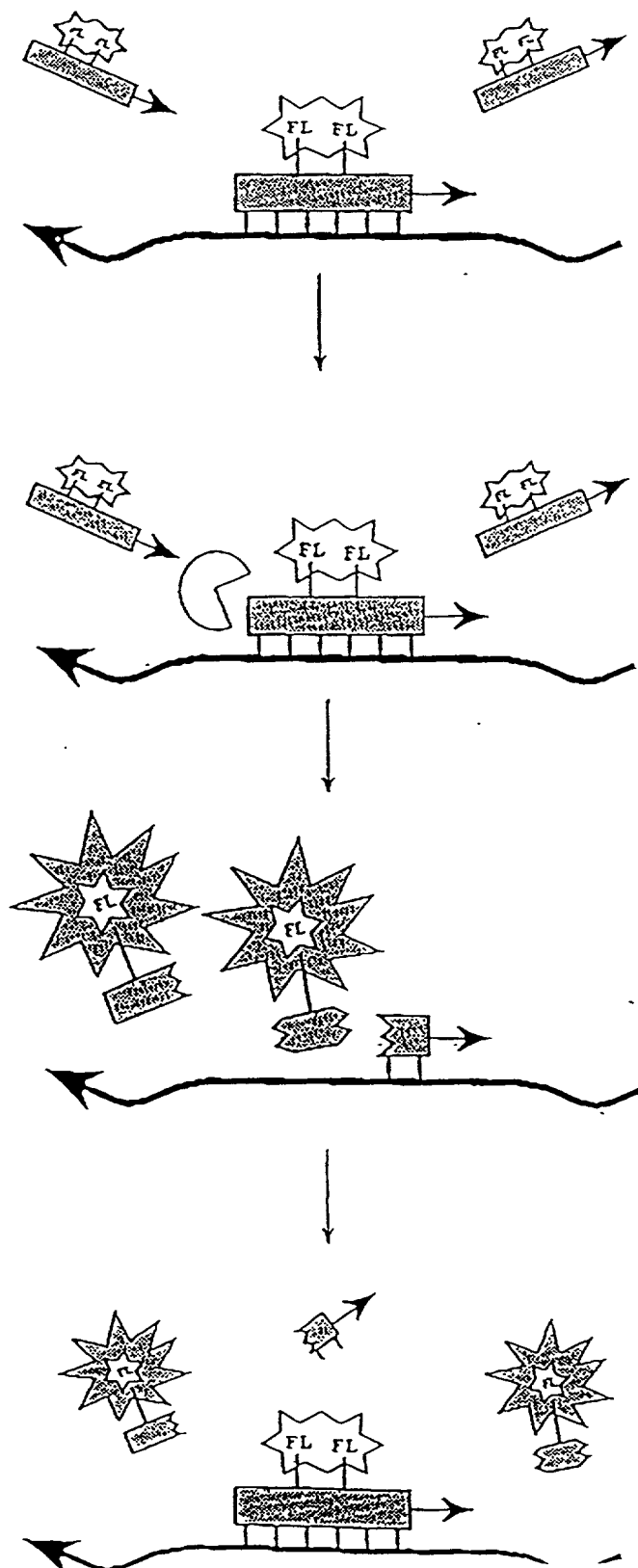
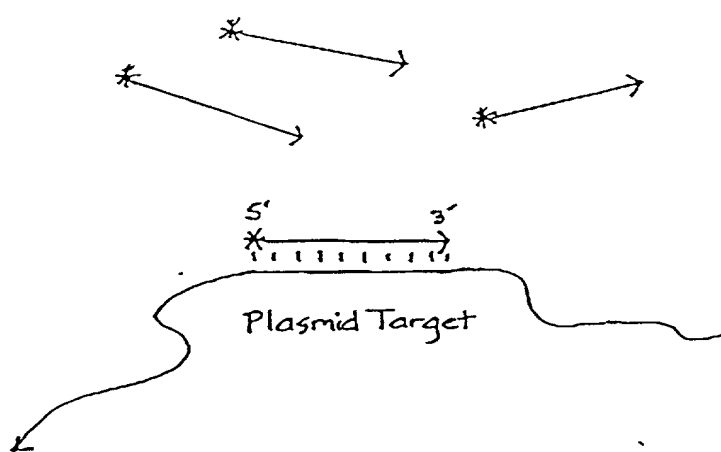


FIGURE 28A



\* =  $^{32}\text{P}$  5' terminal phosphate

FIGURE 28B

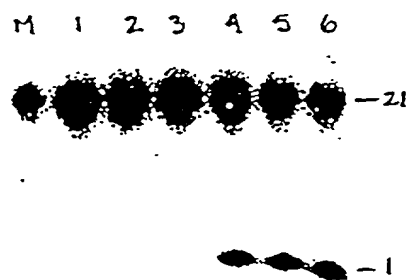




FIGURE 29

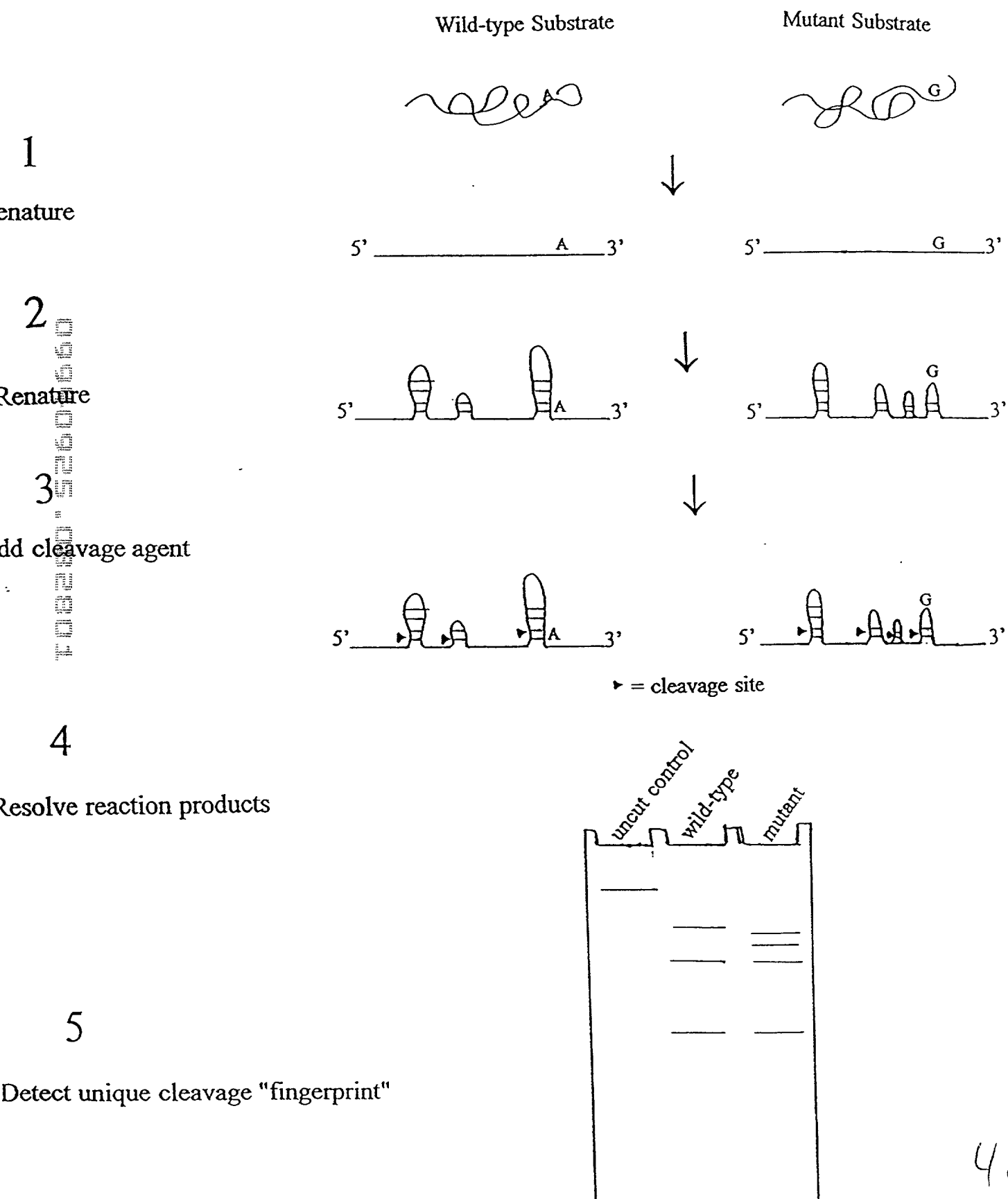
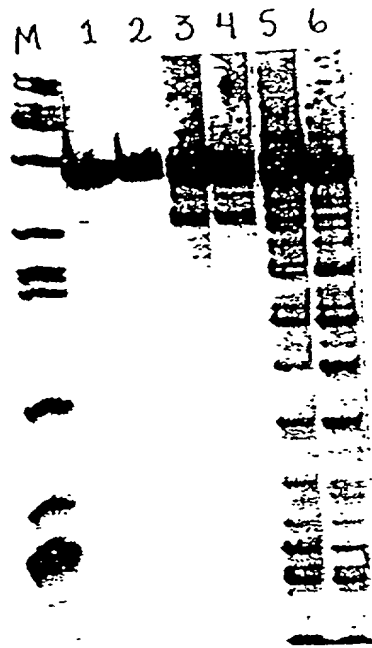


FIGURE 30



004093.0001  
"52604660"

FIGURE 31

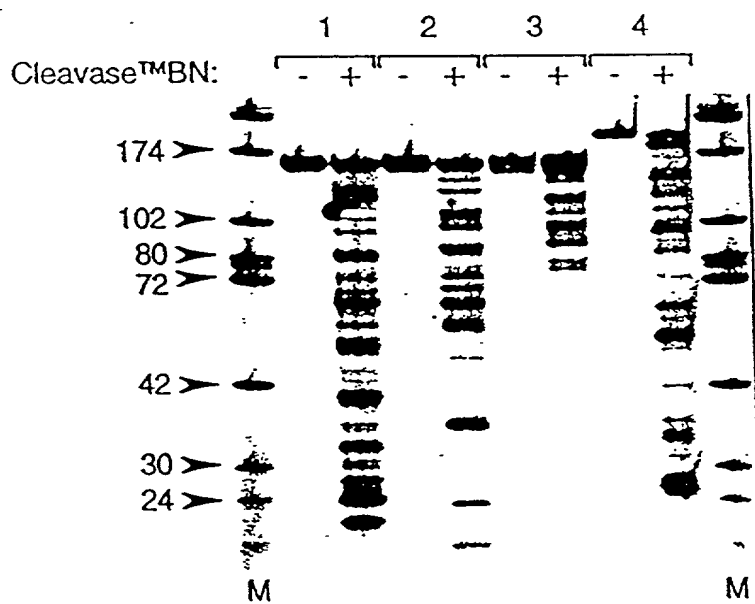


FIGURE 32

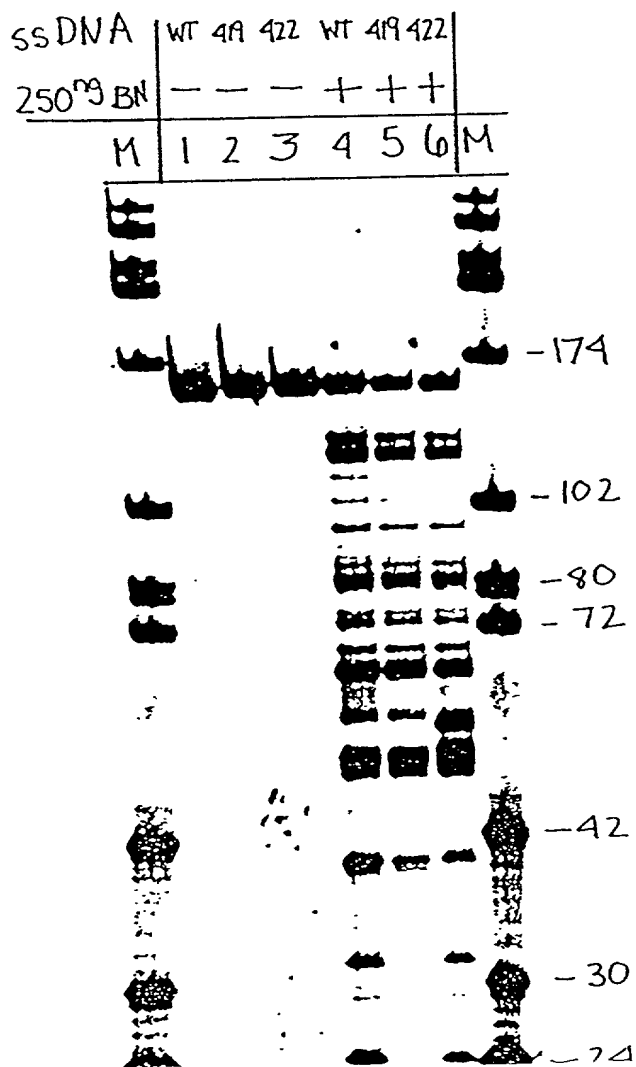


FIGURE 33

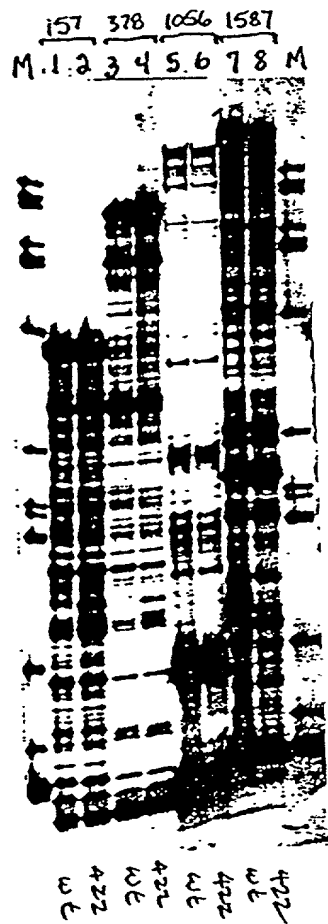


FIGURE 34

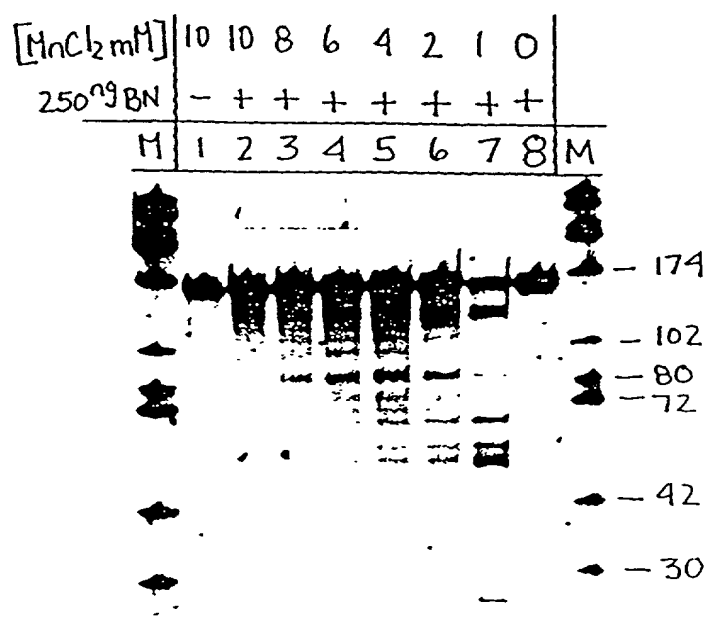


FIGURE 35

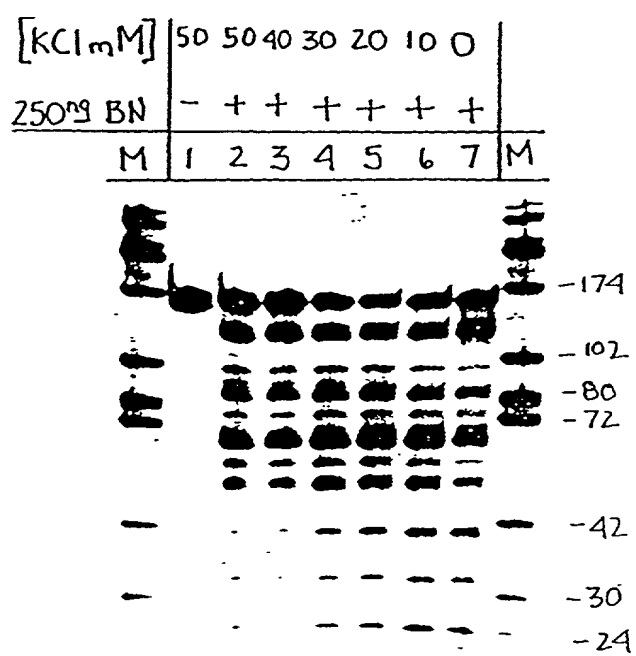


FIGURE 36

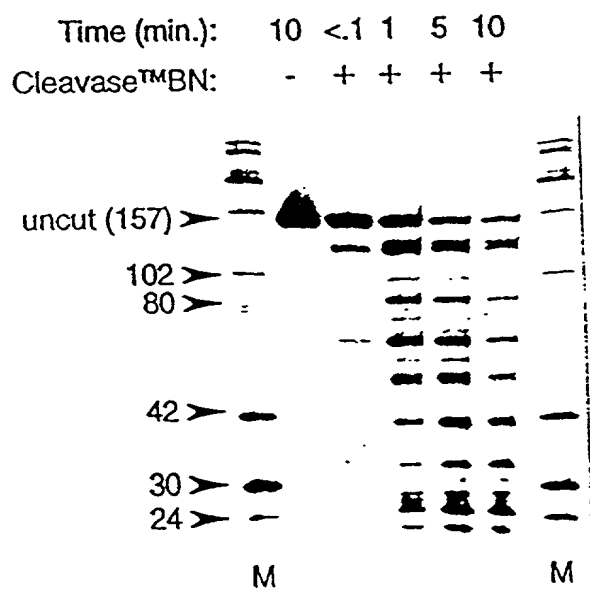




FIGURE 37

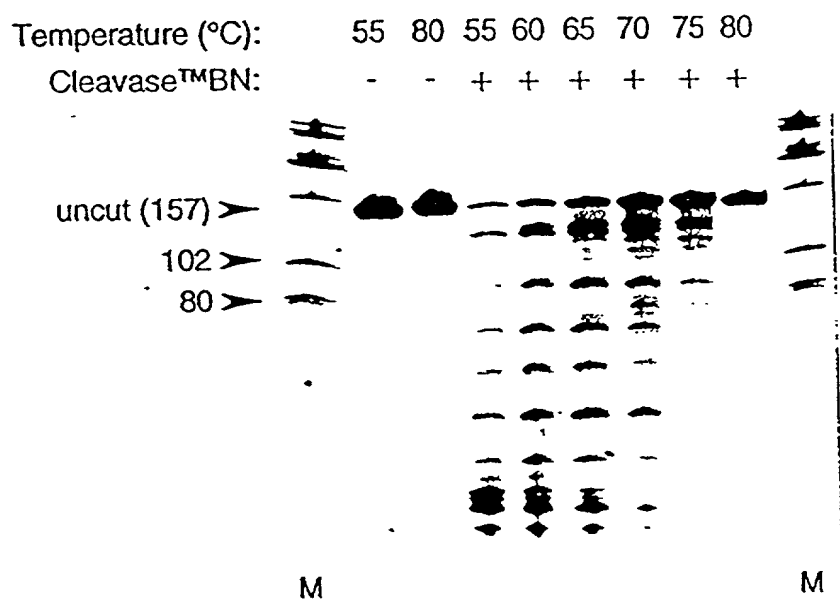




FIGURE 39

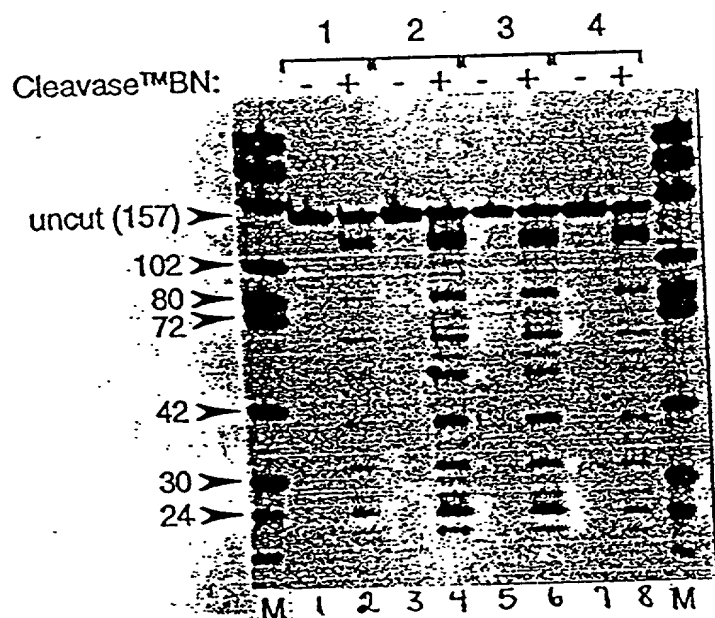
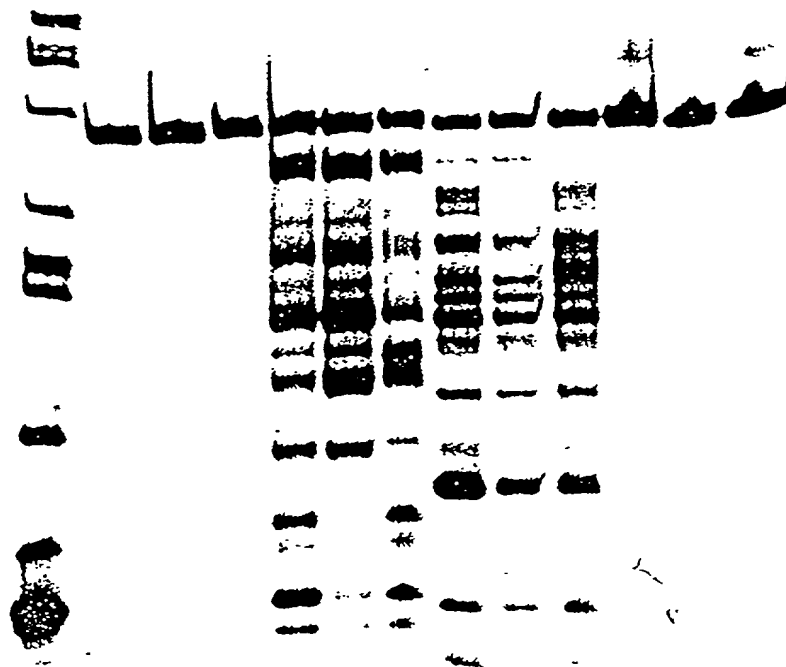


FIGURE 40

strand	5'-BIOTIN SENSE STRAND						5'-FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ss DNA												
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12



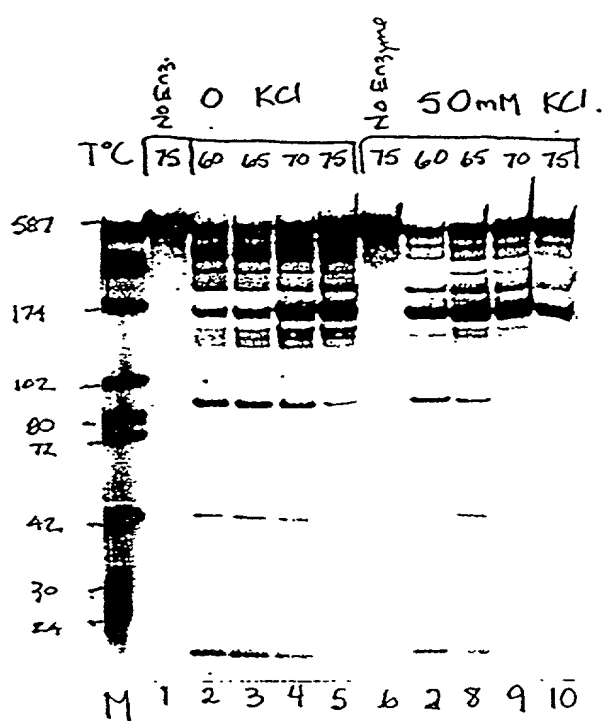


FIGURE 42

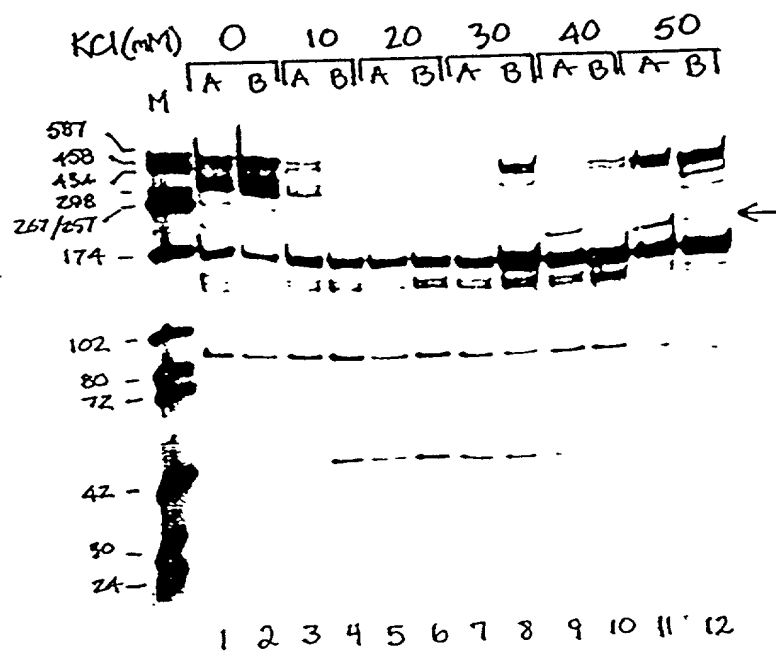


FIGURE 43



FIGURE 44

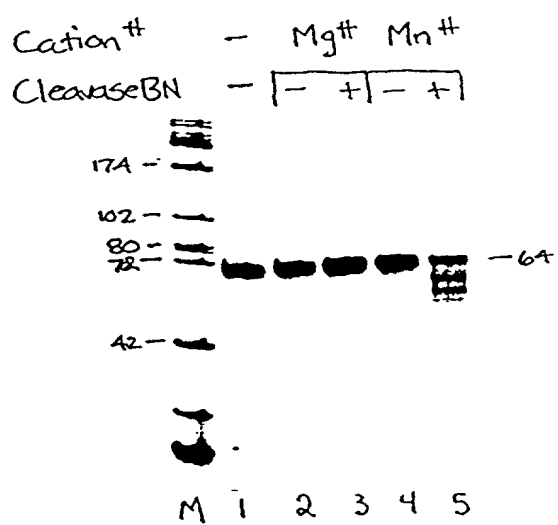




FIGURE 45

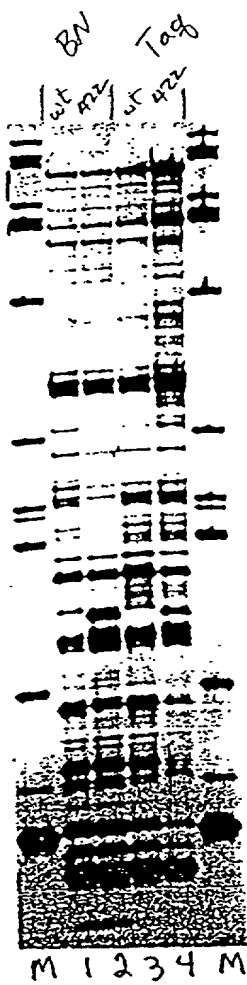


FIGURE 46

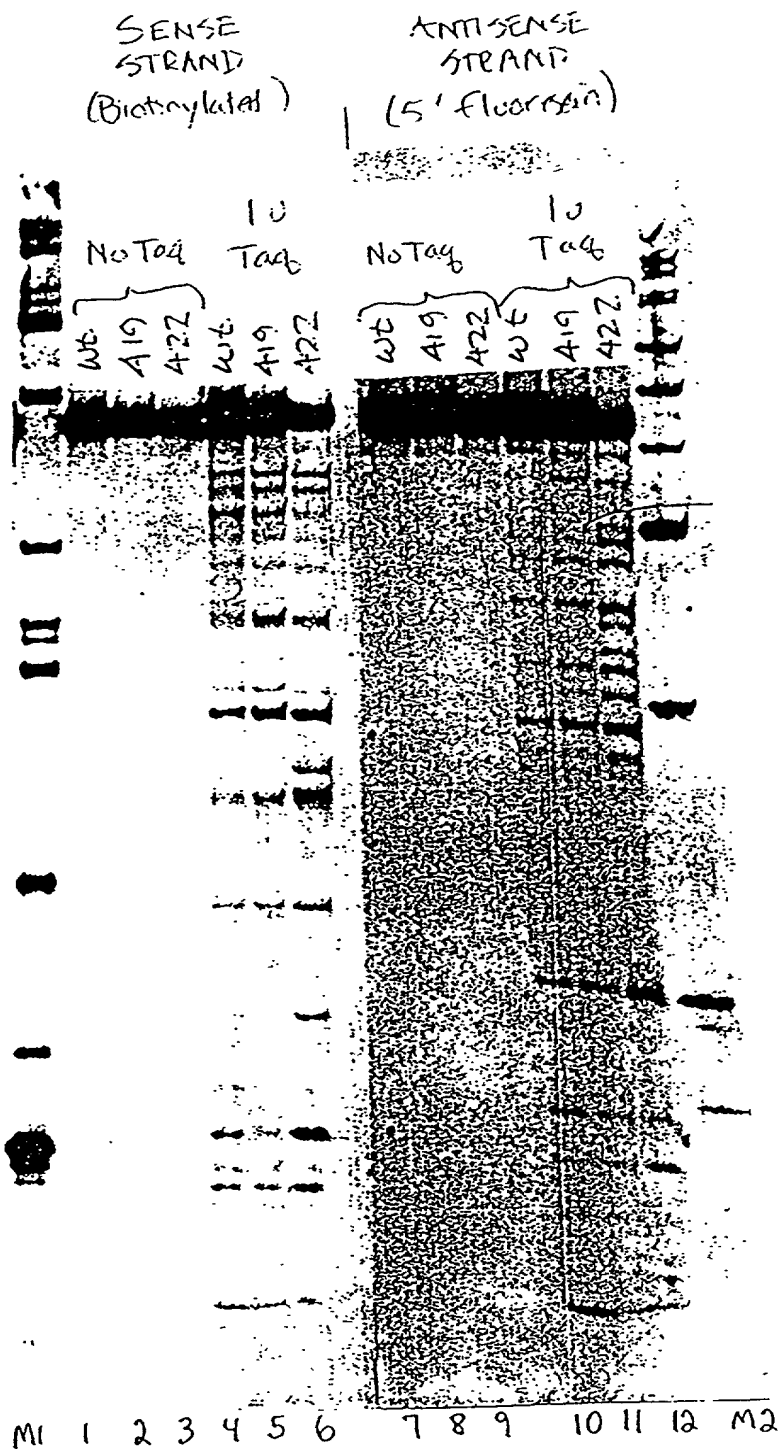
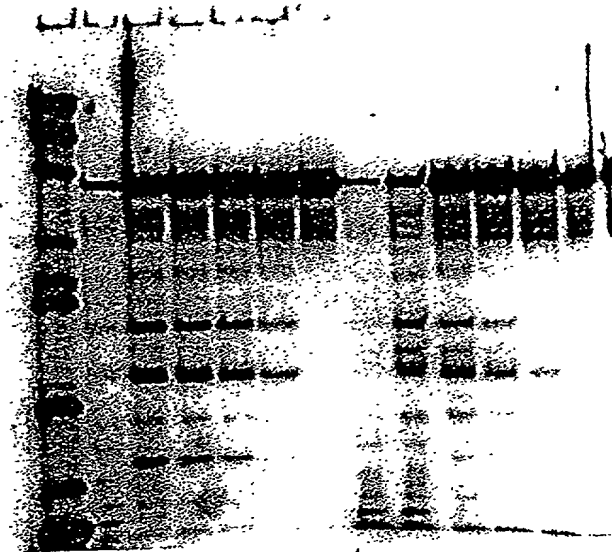


FIGURE 47

419

422

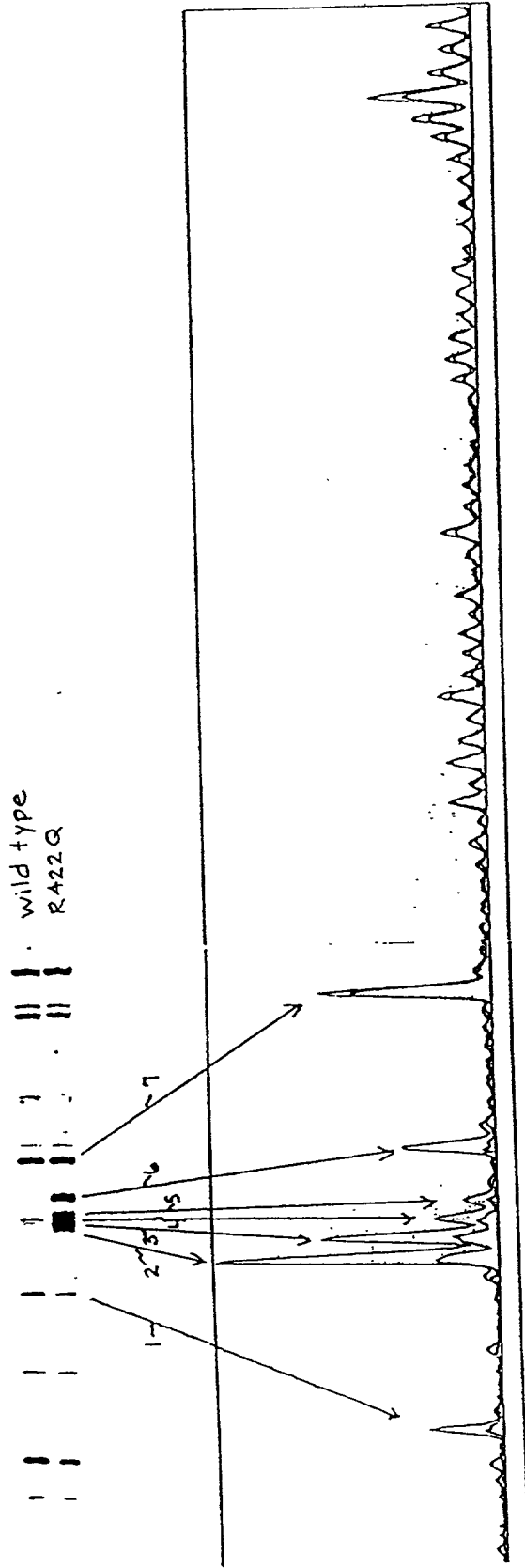
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0.15	0.15
0.10	0.10
0.05	0.05
0.00	0.00



M 1 2 3 4 5 6 7 8 9 10 11 12

094093 02301  
T08280" 52604650

FIGURE 48  
FOE280\*52604650



. 100.8-1 5'GGCTGACAAGAGAAACTCGCTGAGACAGCAGGGACATTTCACCAAGGGG' AUGTTTACCGGGGAGGTTACTGGGGAGGAGCCGGTTCGGGAACGCCCACTCTCT  
1D N0: 76) 3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTGTCCTGAAAGGTGTTCCCC TACAATGCCCTTCCATGACCCCTCTCGGCCAGCCCTTTCGGGCTGAGAGA  
46.16-10 5'GGCTGACAAGAGAAACTCGCTGAGATAGCAGGGACATTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACCCCACTTTCT  
2D N0: 77) 3'CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA  
46.16-12 5'GGCTGACAAGAGAAACTCGCTGAGATAGCAGGGACATTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACCCCACTTTCT  
2D N0: 78) 3'CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA  
19.16-3 5'GGCTGACAAGAGAAACTCGCTGAGACAGCAGGGACATTTCCACAAGGGG ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCTCT  
2D N0: 79) 3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTGTCCTGAAAGGTGTTCCCC TACAATGCCCTTCCATGACCCCTTCCCTCGGCCAGCCCTTTCGGGTGAAAGA  
CEM/251 5'CGCTGACAAGAGAAACTCGCTGAAACAGCAGGGACATTTCCACAAGGGG ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT  
3D N0: 80) 3'CCGACTGTTCTTCCCTTTGAGCGACTTGTGTCCTGAAAGGTGTTCCCC TACAATGCCCTTCCATGACCCCTTCCCTCGGCCAGCCCTTTCGGGTGAAAGA  
36.8-3 5'GGCTGACAAGAGAAACTCGCTGAGACAGCAGGGACATTTCCACAAGGGG ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT  
2D N0: 81) 3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTGTCCTGAAAGGTGTTCCCC TACAATGCCCTTCCATGACCCCTTCCCTCGGCCAGCCCTTTCGGGTGAAAGA  
100.8-1 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGACCCCTCCAAAGAGAGGTCTGTGATCGTCCCATC  
46.16-10 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGACCCCTCCAAAGAGAGGTCTGTGATCGTCCCATC  
46.16-12 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGACCCCTCCAAAGAGAGGTCTGTGATCGTCCCATC  
19.16-3 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGACCCCTCCAAAGAGAGGTCTGTGATCGTCCCATC  
CEM/251 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGACCCCTCCAAAGAGAGGTCTGTGATCGTCCCATC  
36.8-3 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT CTCGACCCGTCTAACTCGGAGATCTCCAAAGAGAGGTCTGTGATCGTCCCATC

61

L. 100.8-1 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACAGCAGCTTGGCCGGTGGTGGG CAGAGTGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 76) 3' TCGGACCCCAAGGACGATCTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCACCGAGGTGGACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

L. 46.16-10 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACAGCAGCTTAGCCAGTGGTGGG CAGAGTGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 77) 3' TCGGACCCCAAGGACGATCTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCACCGAGGTGGACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

L. 46.16-12 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACAGCAGCTTGGCCAGTGGTGGG CAGAGTGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 78) 3' TCGGACCCCAAGGACGATCTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCACCGAGGTGGACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

L. 19.16-3 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACAGCAGCTTGGCCGGTGGTGGG CAGAGTGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 79) 3' TCGGACCCCAAGGACGATCTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCACCGAGGTGGACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

L. CEM/251 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACAGCAGCTTGGCCGGTGGTGGG CAGAGTGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 80) 3' TCGGACCCCAAGGACGATCTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCACCGAGGTGGACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

L. 36.8-3 5' AGCCTGAGTGTTCCTGCTAAACTCTCACAGCAGCTTGGCCGGTGGTGGG CAGAGCGGCTCCACGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
(Seq ID NO: 81) 3' TCGGACTCACAGGACGATTTGAGAGTGGTGGTAAACCGGCCACGACCC GTCTCGCCGAGGTGGCAACGAACGAATTTCTGGAGAAAGTTATTTTCGACGG

350

L. 100.8-1 5' ATTTTAGAAGTAGGCCAGTGTGTGTTCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACACAGGGTAGAGGATCGGCGCGGAC C 5'

L. 46.16-10 5' ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACAGGGTAGAGGATCGGCGCGGAC C 5'

L. 46.16-12 5' ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACAGGGTAGAGGATCGGCGCGGAC C 5'

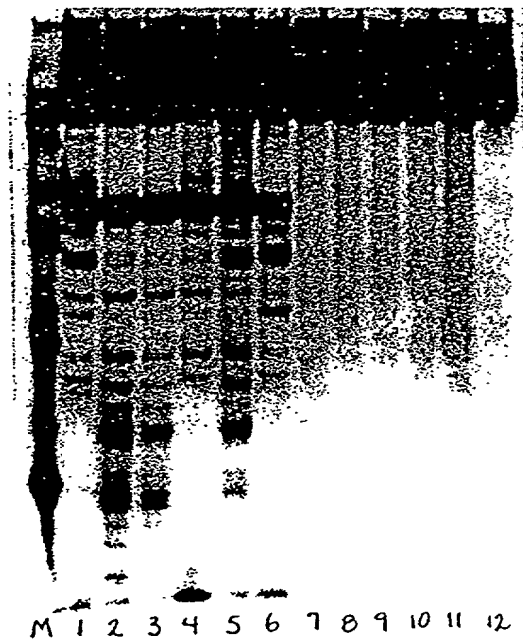
L. 19.16-3 5' ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACAGGGTAGAGGATCGGCGCGGAC C 5'

L. CEM/251 5' ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACAGGGTAGAGGATCGGCGCGGAC C 5'

L. 36.8-3 5' ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCGCGCCCTG G 3'  
3' TAAATCTTCATCCGTTCAACACACAGGGTAGAGGATCGGCGCGGAC C 5'

62

FIGURE 50



T03280" 52604650

FIGURE 51

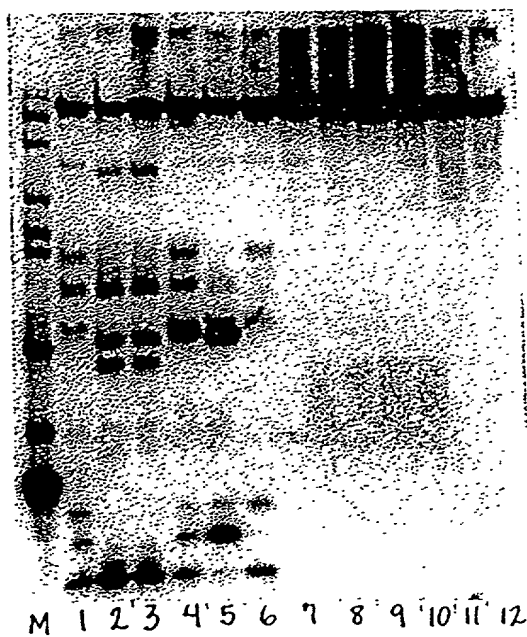
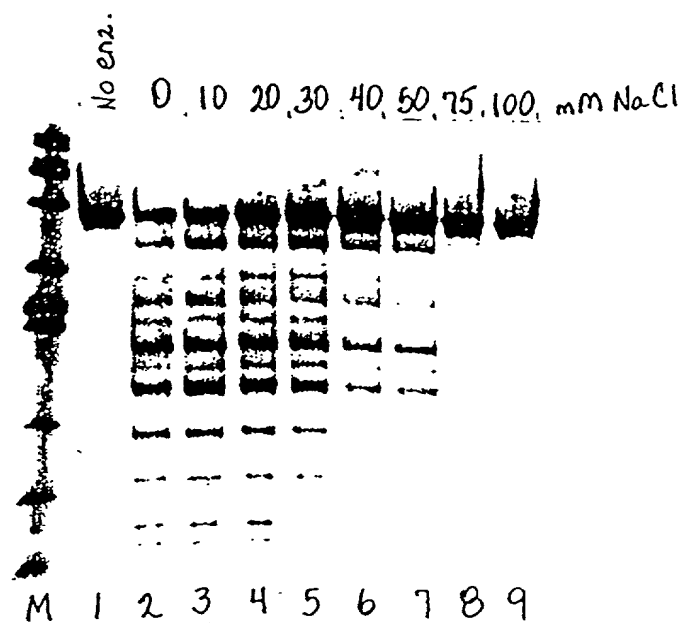


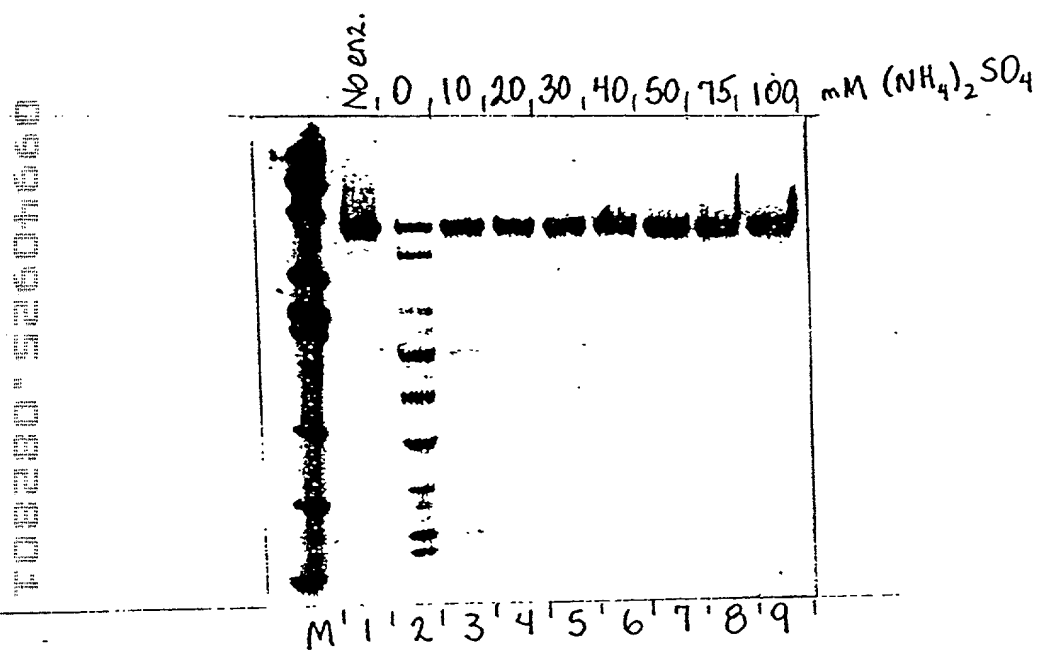


FIGURE 52



65

FIGURE 53



T08280"52604650

FIGURE 54

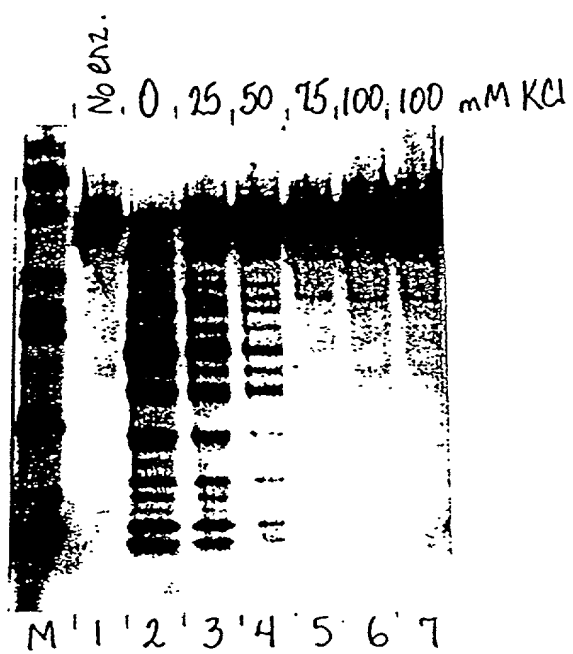


FIGURE 55

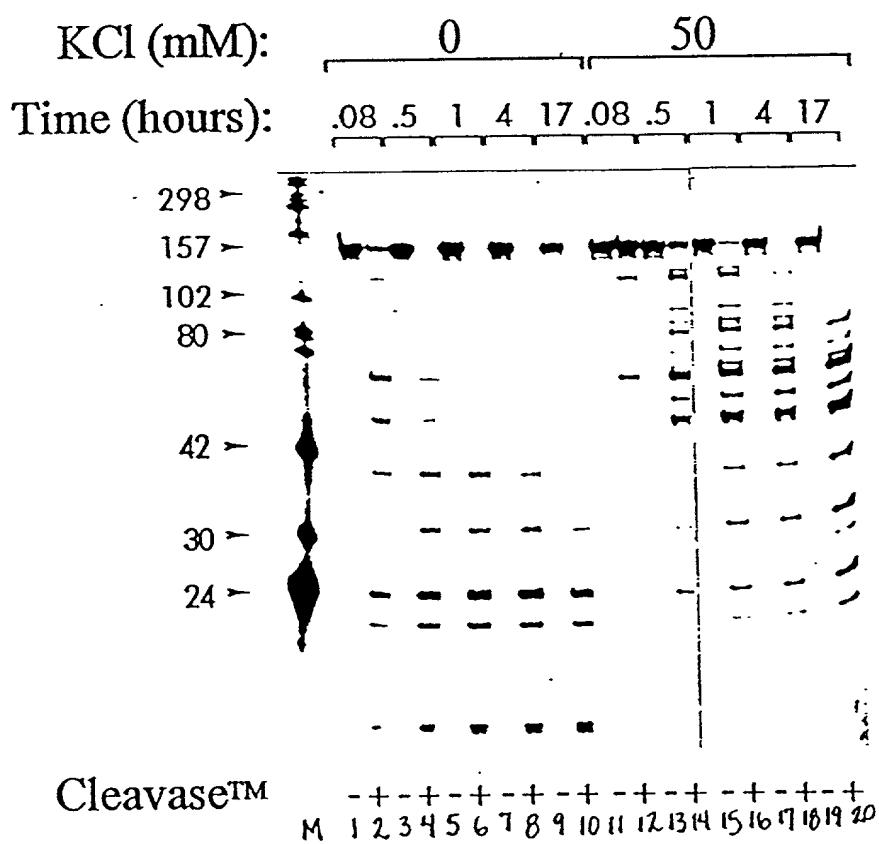


FIGURE 56

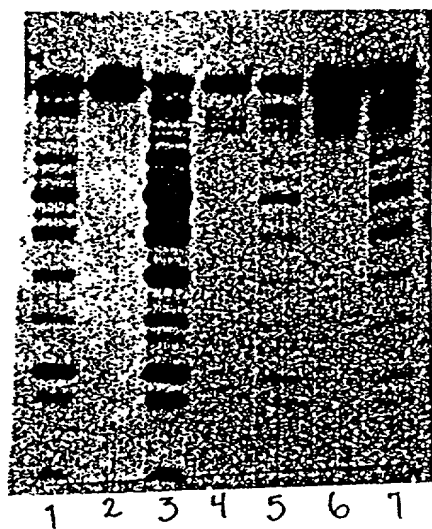
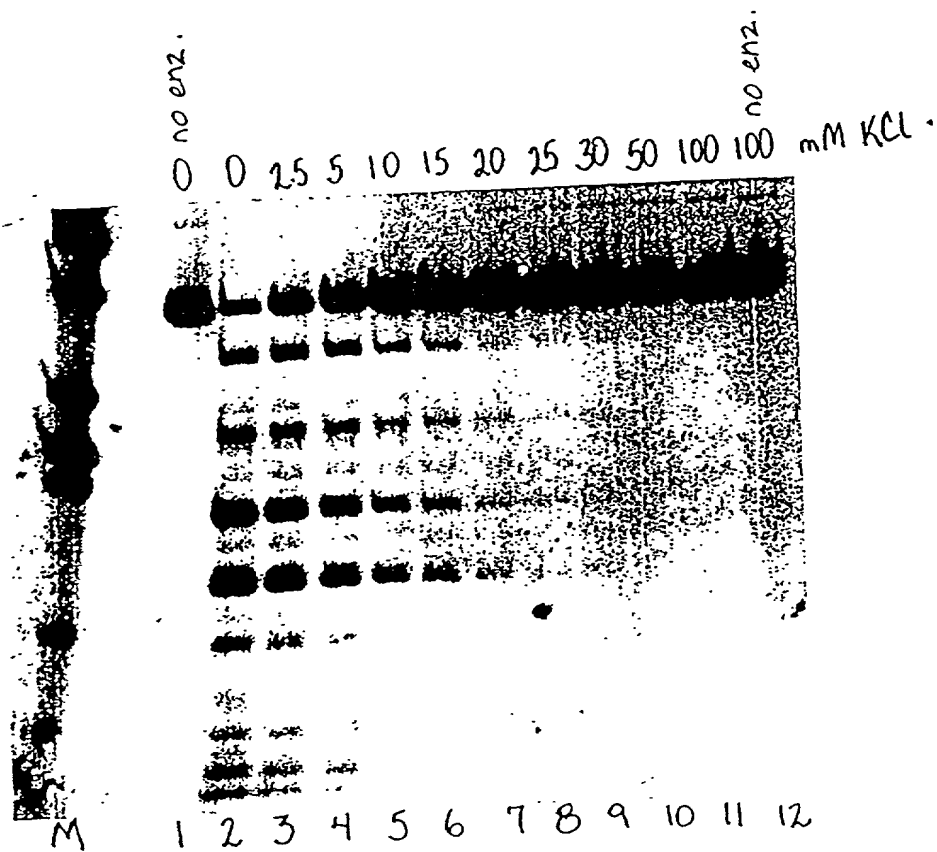


FIGURE 57



094493 09604650

FIGURE 58

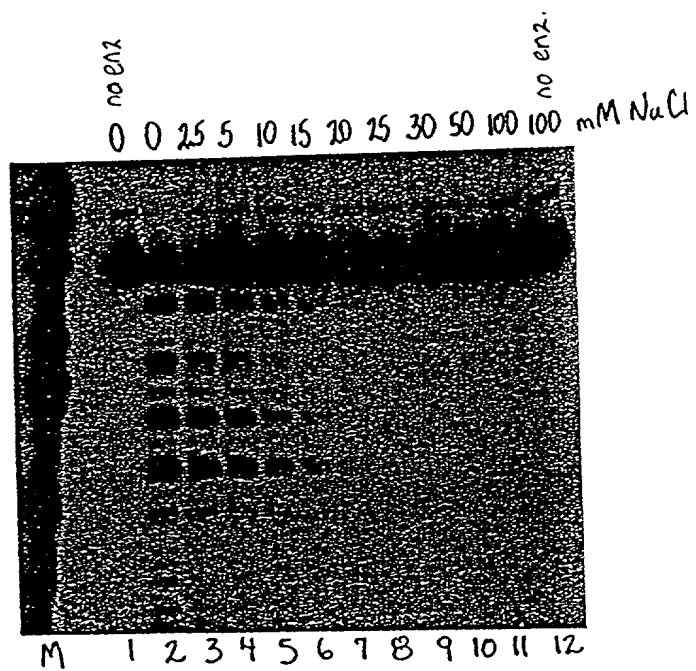
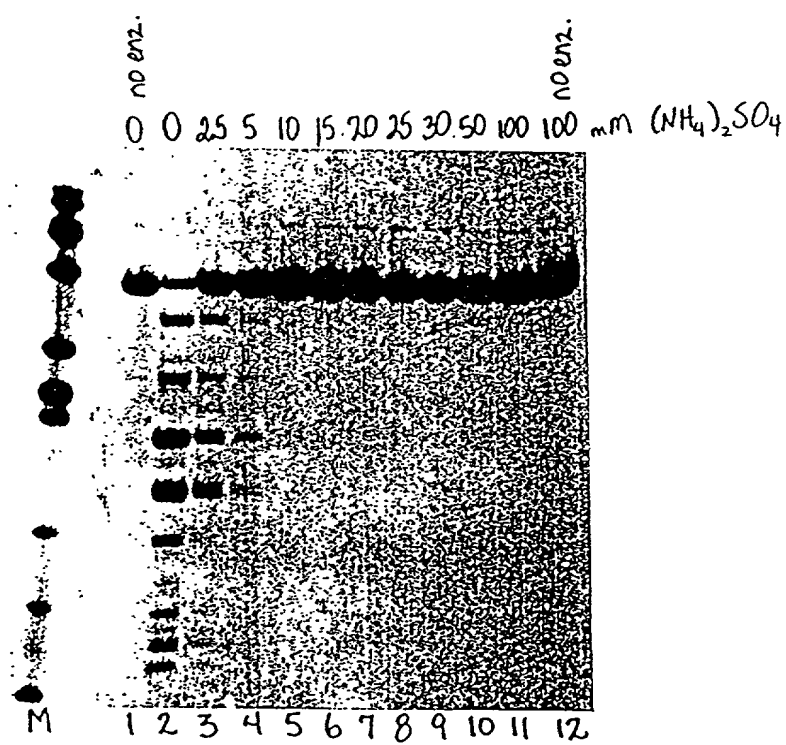


FIGURE 59





108280" 52604660

FIGURE 60

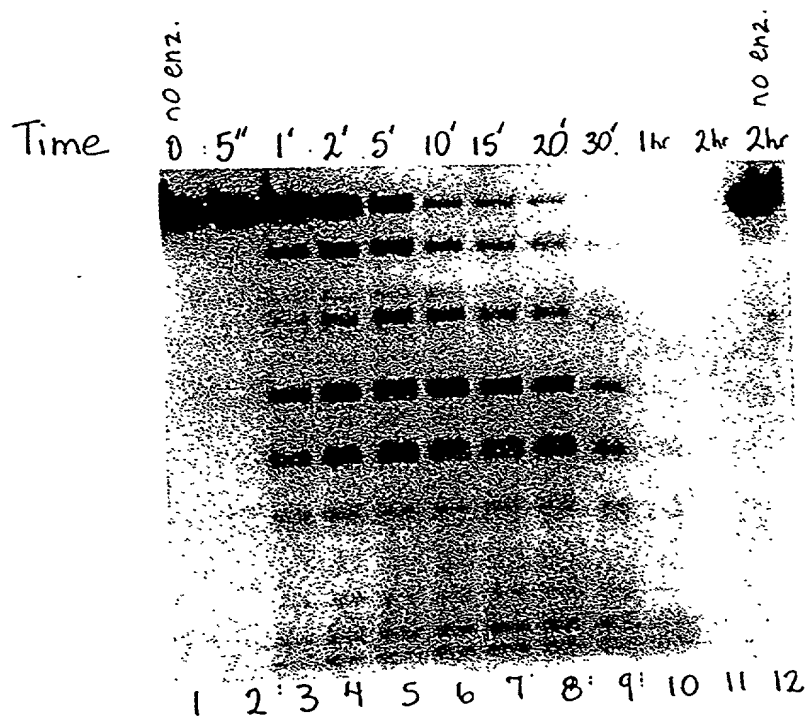


FIGURE 61

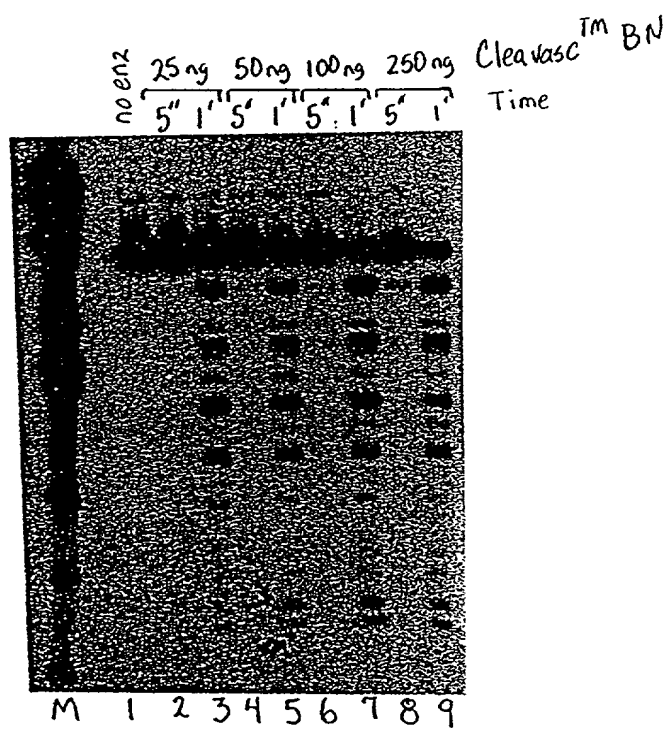


FIGURE 62

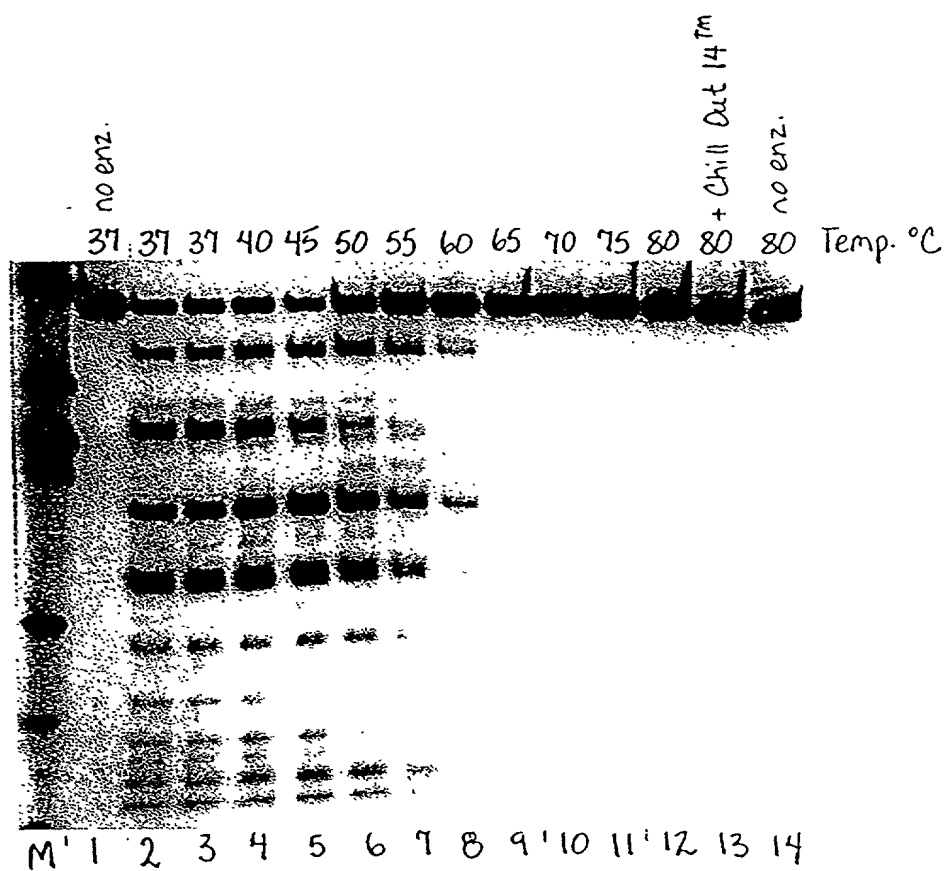


FIGURE 63

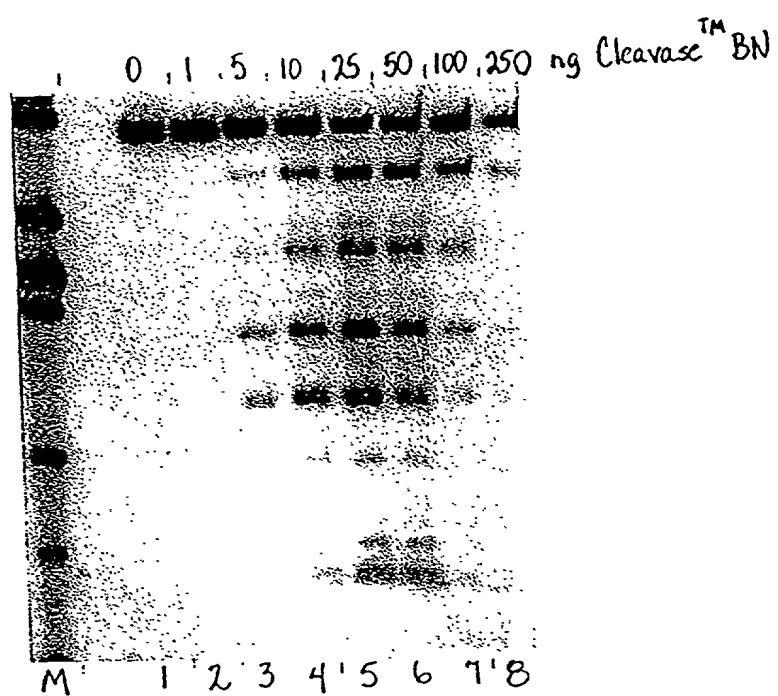
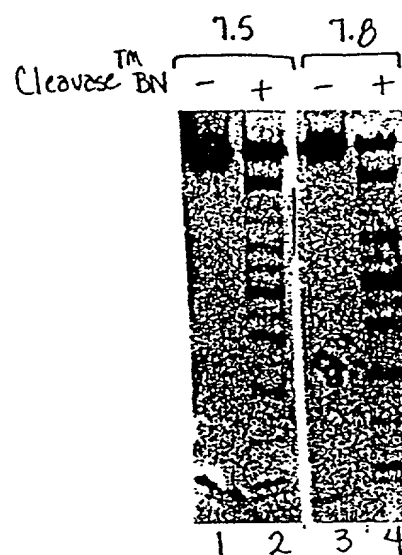
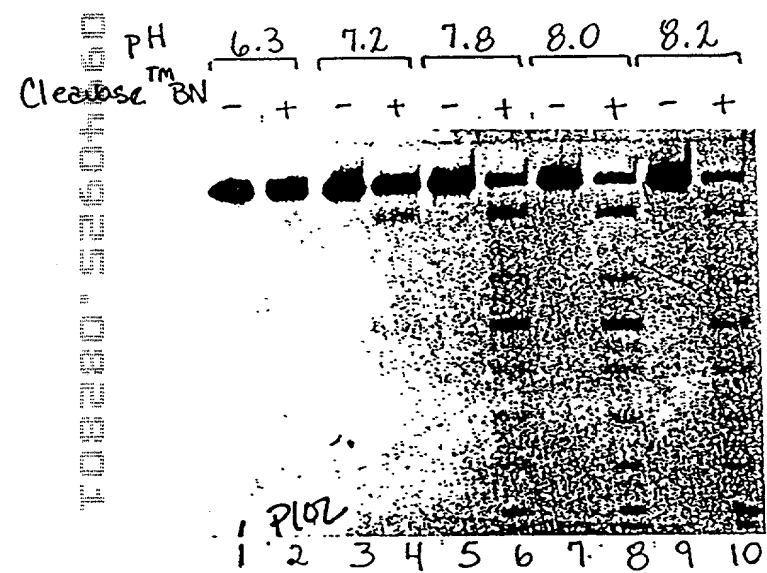


FIGURE 64

A

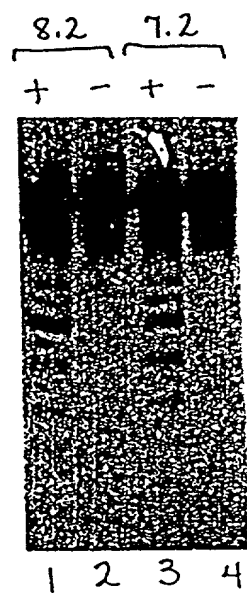
B



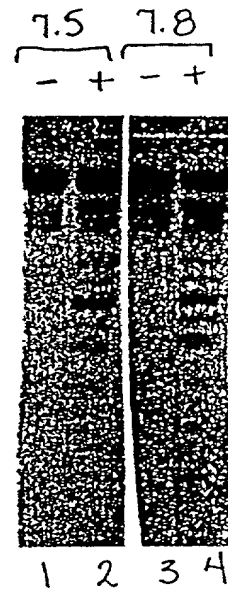
# FIGURE 65

A

B



pH  
Cleavase™ BN



FOU280" 92604650

FIGURE 66

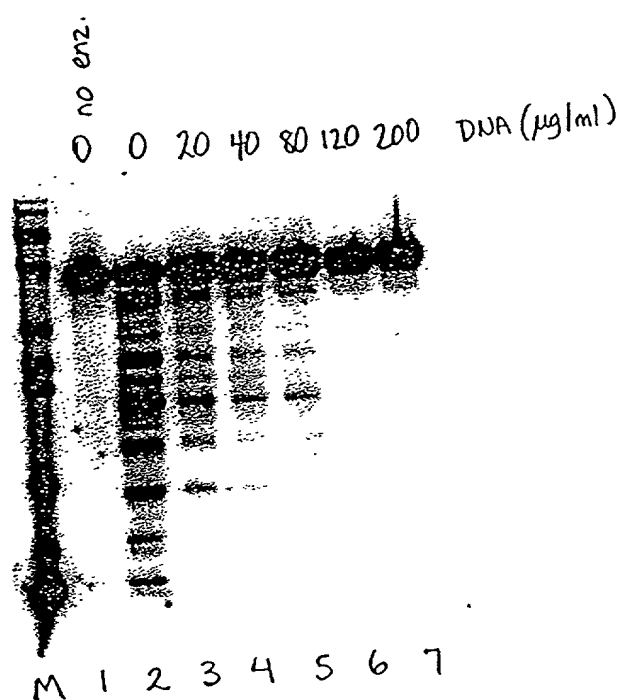
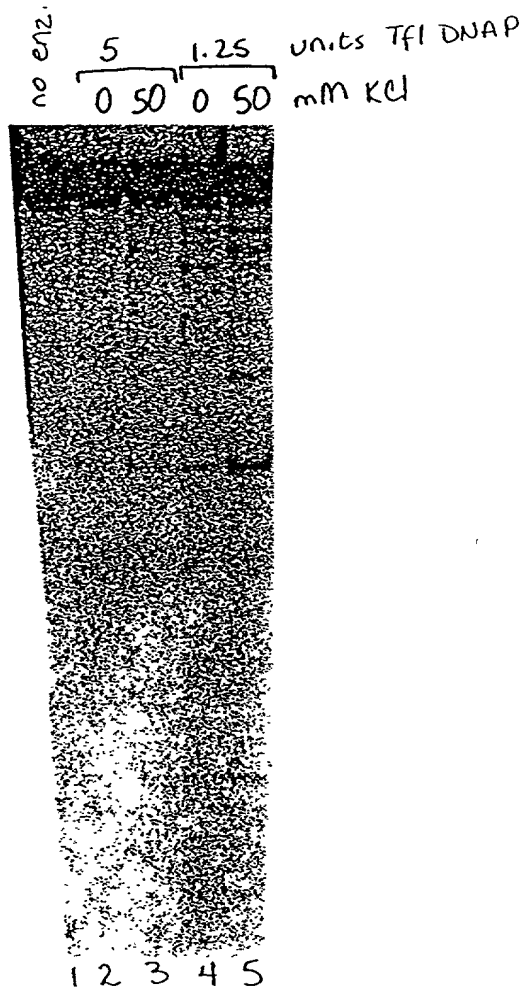


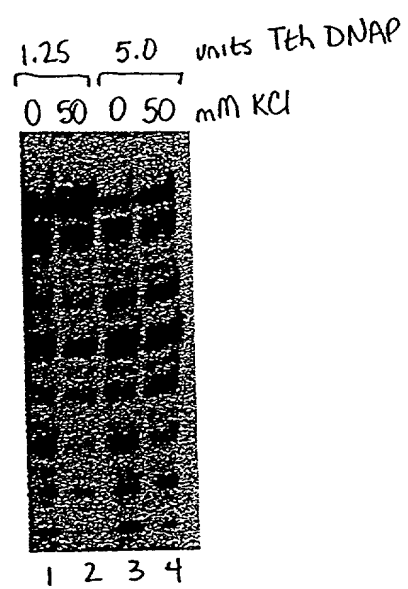
FIGURE 67





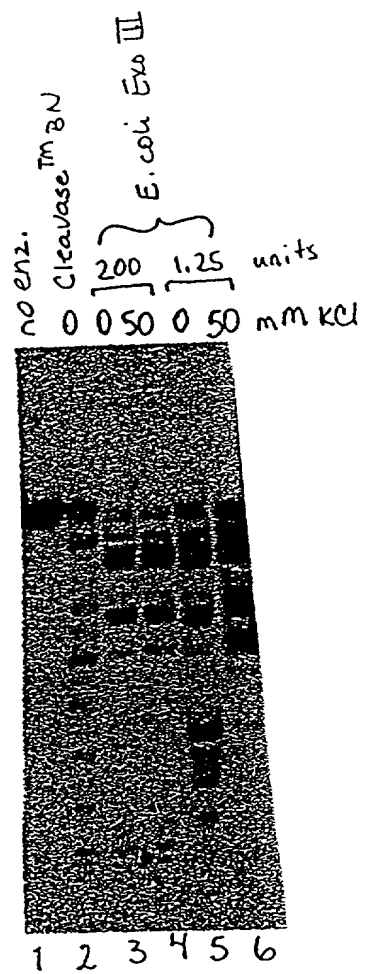
034030 52504650

FIGURE 68



TOP220" 52504660

FIGURE 69



102280 52604660

FIGURE 70

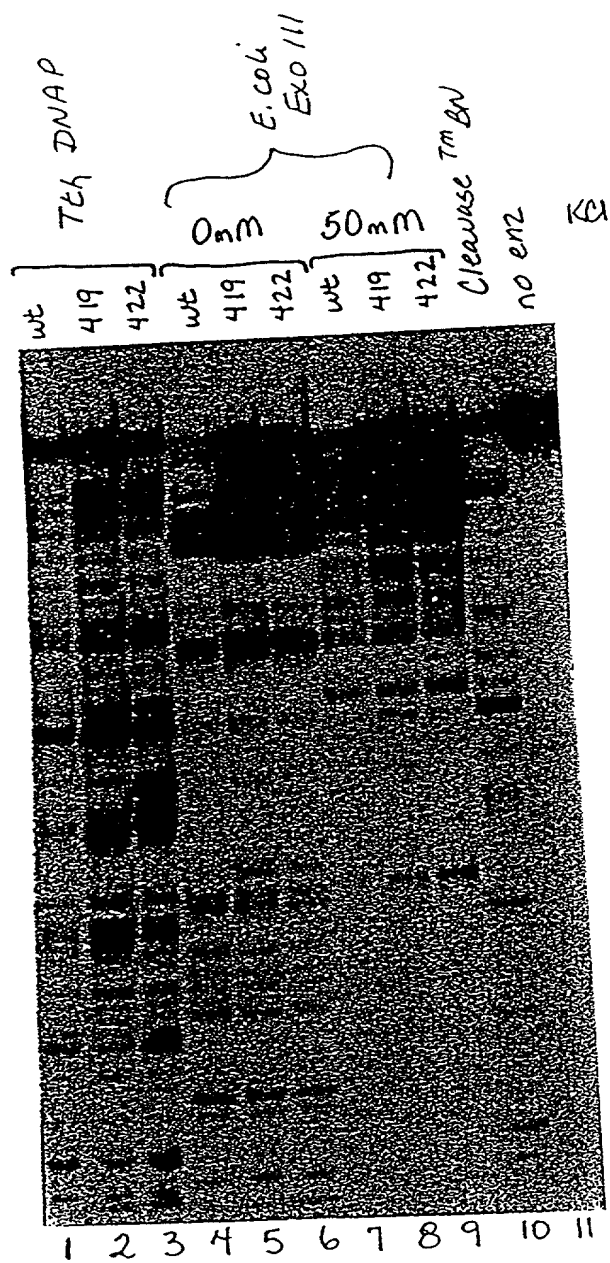


FIGURE 71

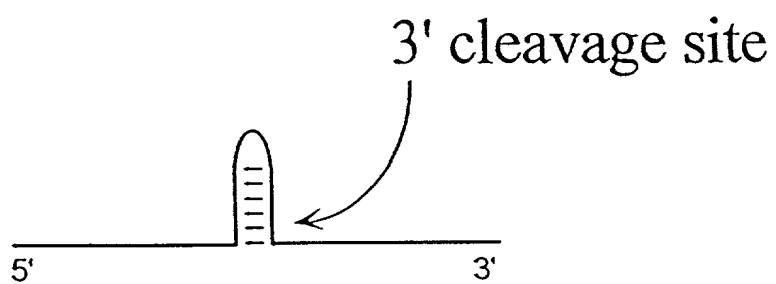
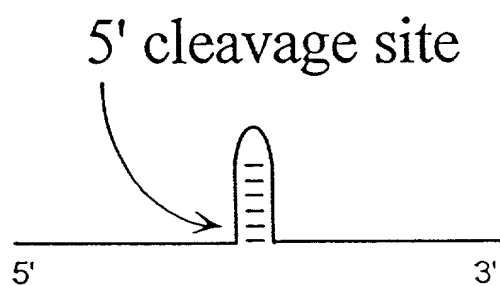


FIGURE 72

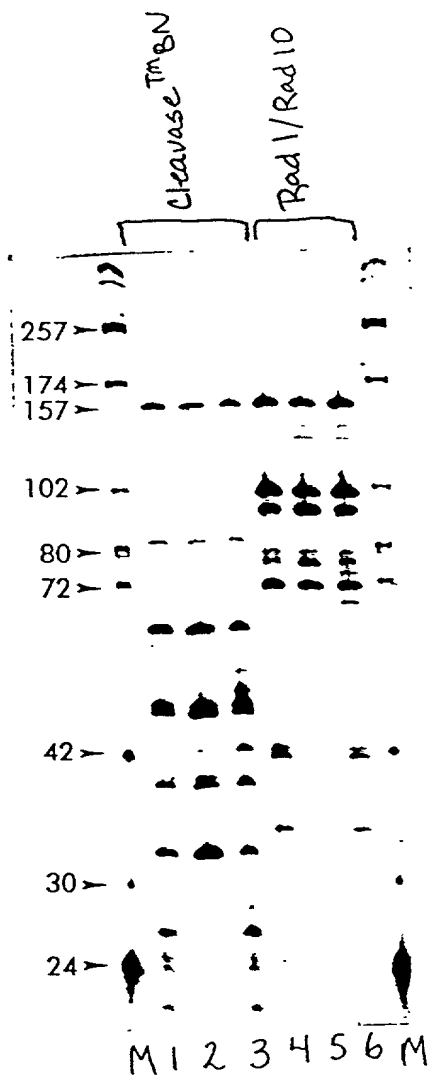


FIGURE 73

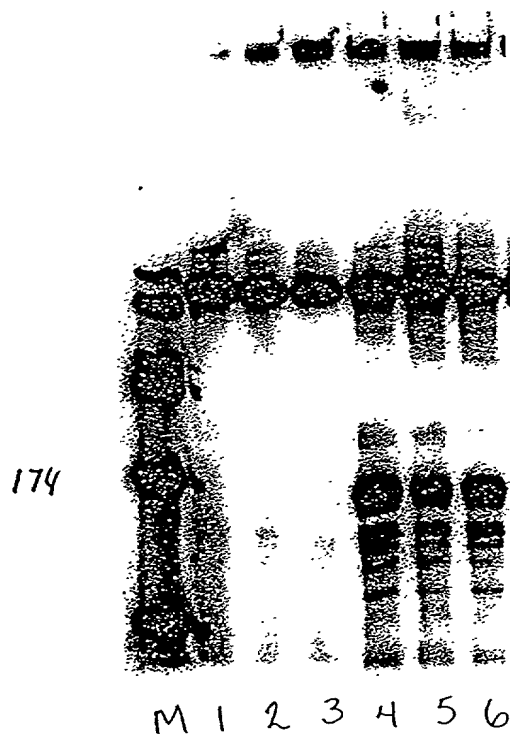
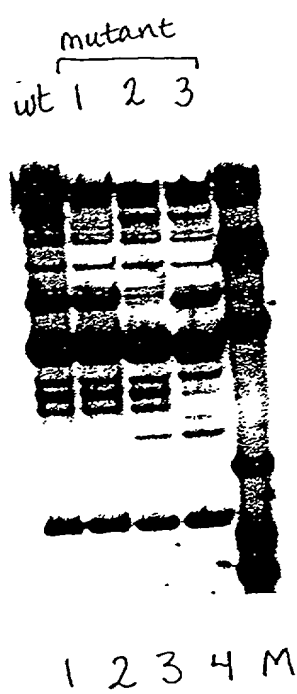
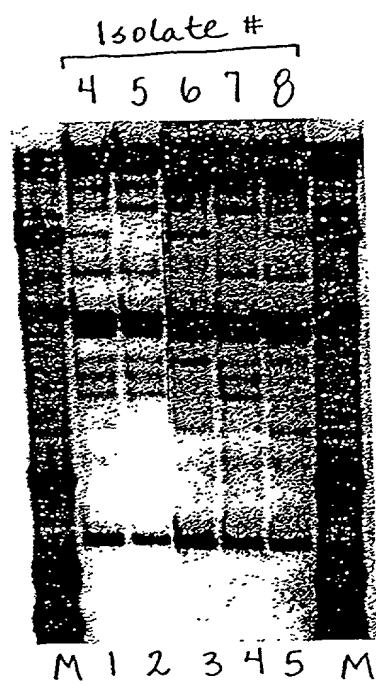


FIGURE 74

A



B



FO3230" 5260450

FIGURE 75

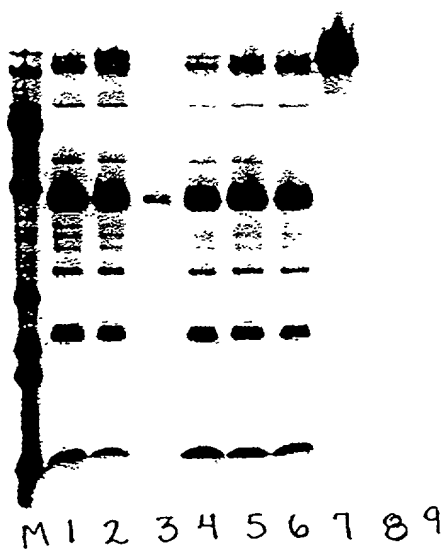




FIGURE 76

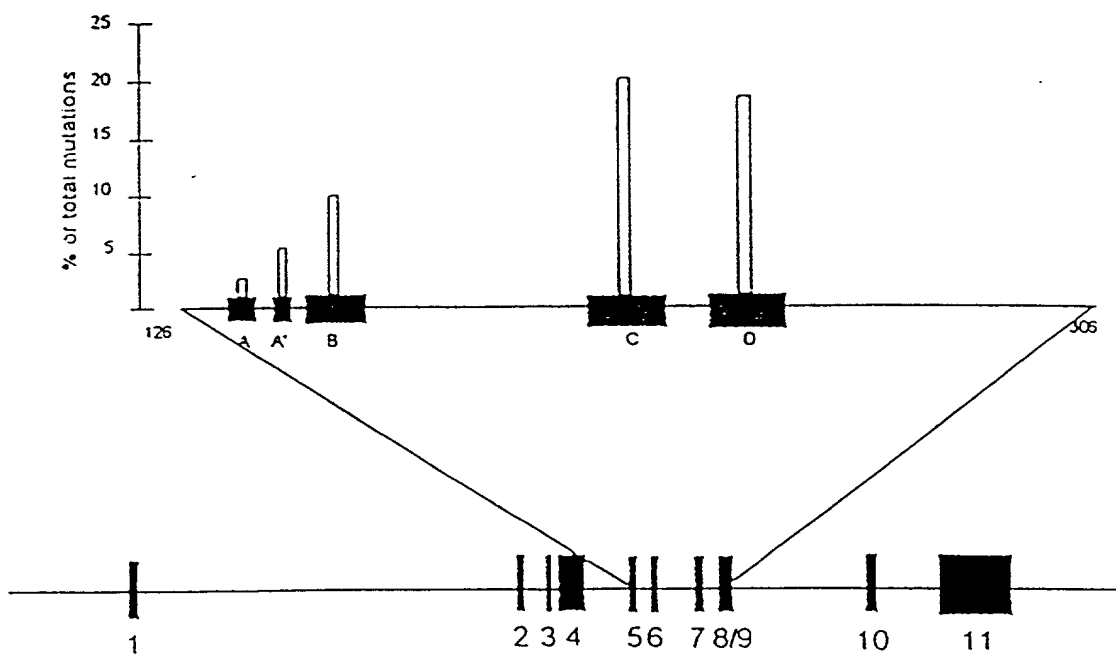


FIGURE 77

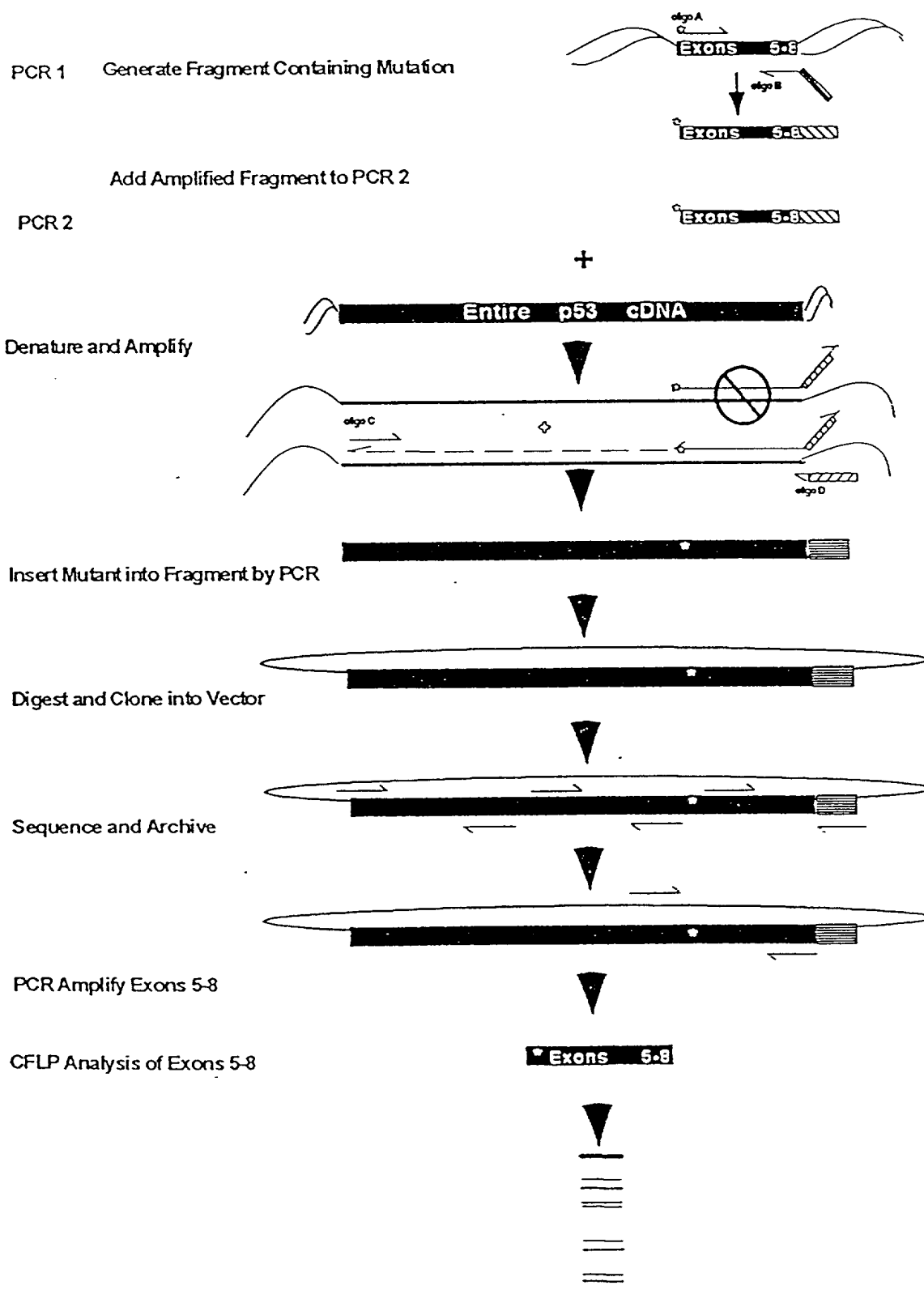
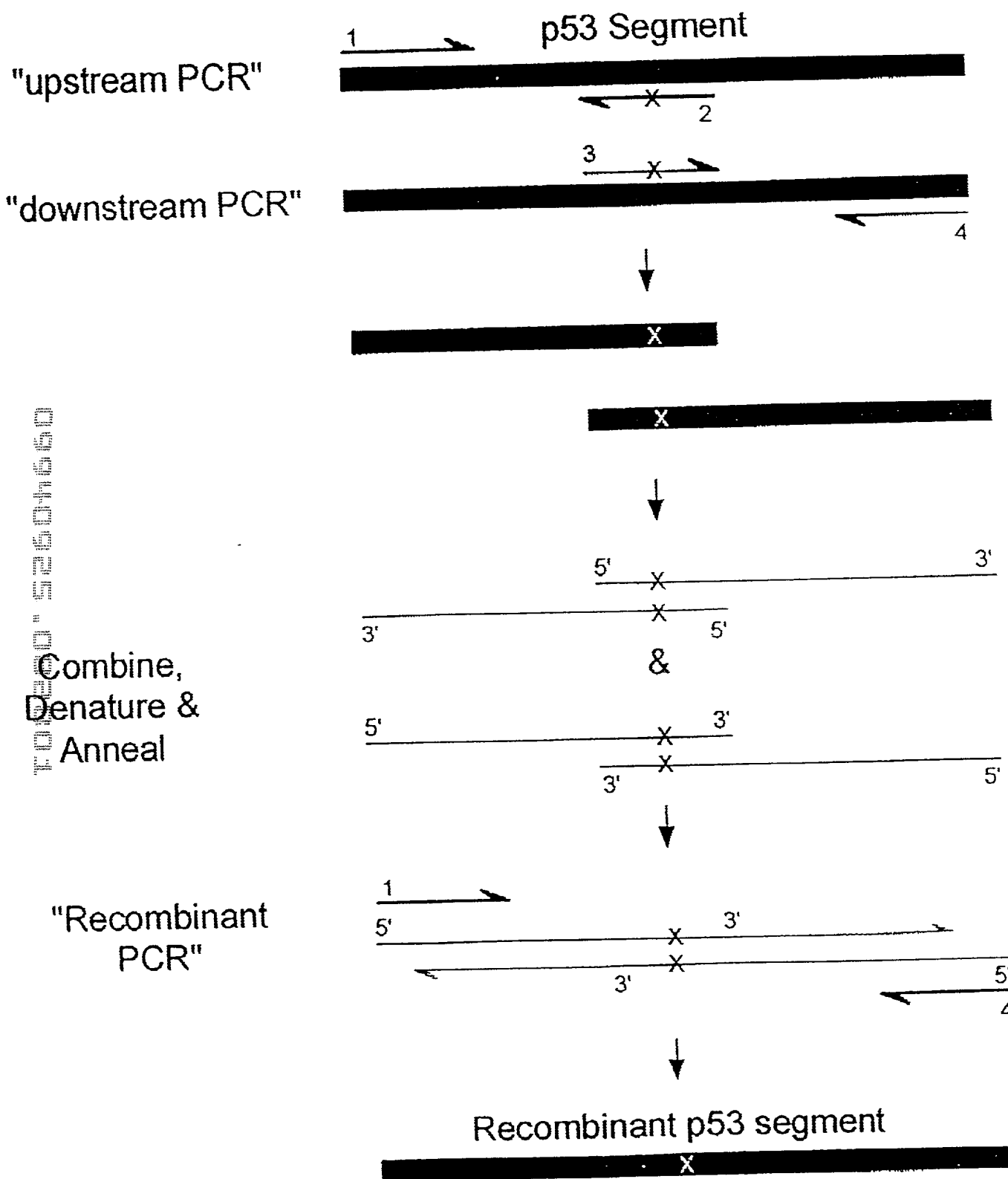


FIGURE 78



FOB280" 52607560

FIGURE 79

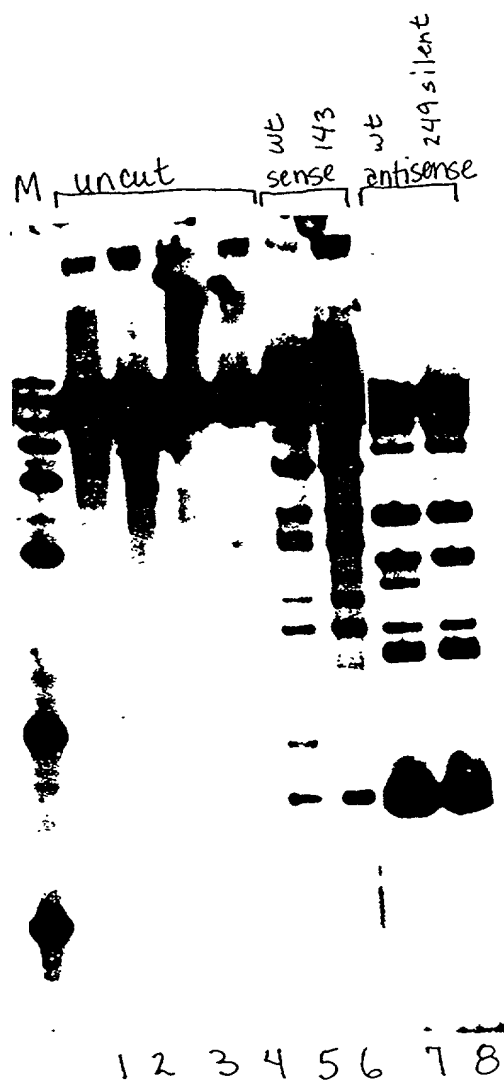
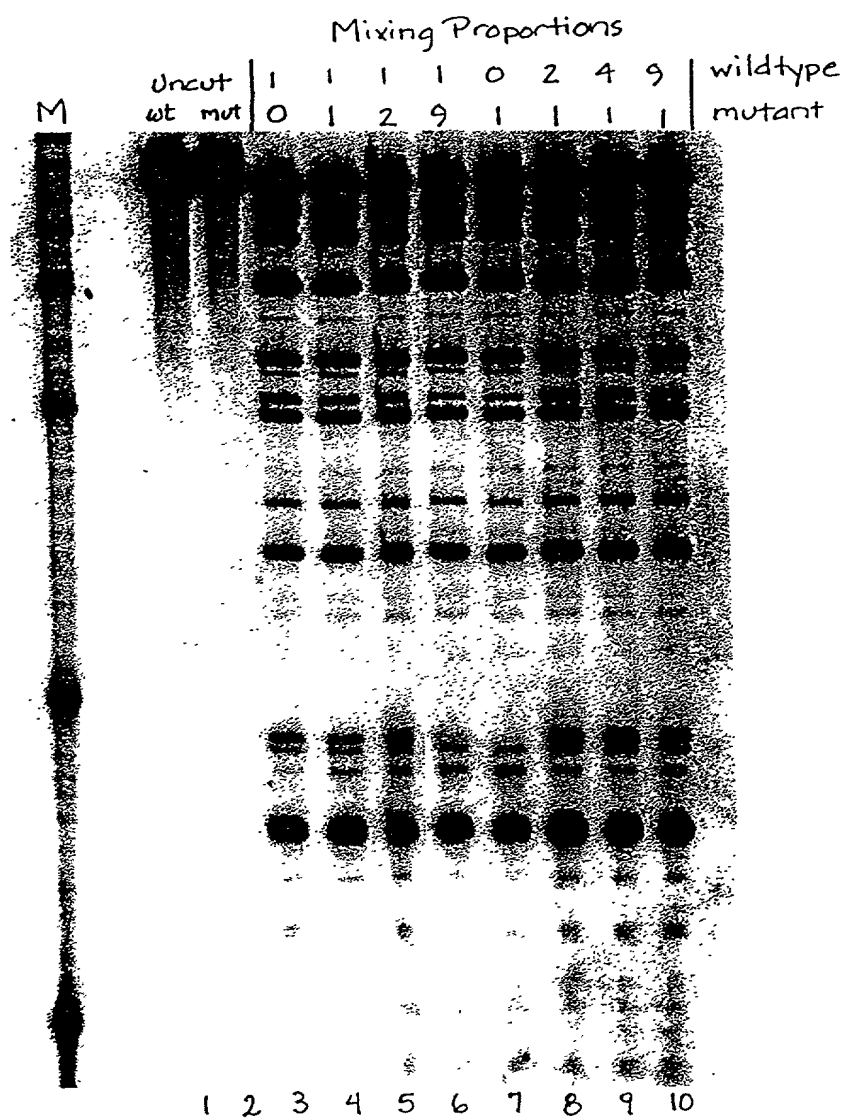


FIGURE 80



FIGURE 81



# FIGURE 82

HCV1.1 (SEQ ID NO:121)  
HCV2.1 (SEQ ID NO:122)  
HCV3.1 (SEQ ID NO:123)  
HCV4.2 (SEQ ID NO:124)  
HCV6.1 (SEQ ID NO:125)  
HCV7.1 (SEQ ID NO:126)

1 CTGCTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTGT 50  
CTGCTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT  
CTGCTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT  
CTGCTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT  
CTGCTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT  
CTGCTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAT GAGTGTCTGT  
51 CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC 100  
CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCT CCGGGAGAG CCATAGTGT CTGCGGAACC

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

101 GGTGAGTACA CCGGAATTGC CAGGACGACC GGTCTCTTTC TTGGAT-AAA 150  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGTCTCTTTC TTGGAT-CAA  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGTCTCTTTC TTGGAT-CAA  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGTCTCTTTC GTGGATGTAA  
GGTGAGTACA CCGGAATTGC CGGGAAGACT GGTCTCTTTC TTGGAT-AAA  
GGTGAGTACA CCGGAATTGC TGGGTGACC GGTCTCTTTC TTGGAG-CAA

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

151 CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCGCAAGA CTGCTAGCCG 200  
CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCGCAAGA CTGCTAGCCG  
CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCGCAAGA CTGCTAGCCG  
CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCGCAAGA CTGCTAGCCG  
CCCACTCTAT GCCCGGCCAT TTGGGCGTGC CCCGCAAGA CTGCTAGCCG  
CCCGCTCAAT ACCCAGAAAT TTGGGCGTGC CCCGCAAGA TCACTAGCCG

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

201 AGTAGTGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT 250  
AGTAGTGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT  
AGTAGTGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT  
AGTAGTGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT  
AGTAGCGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT  
AGTAGTGTG GGTGCGGAAA GGCTTGTGG TACTGCCTGA TAGGGTGCCT

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

251 GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC 282  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTACCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC

5

FIGURE 83

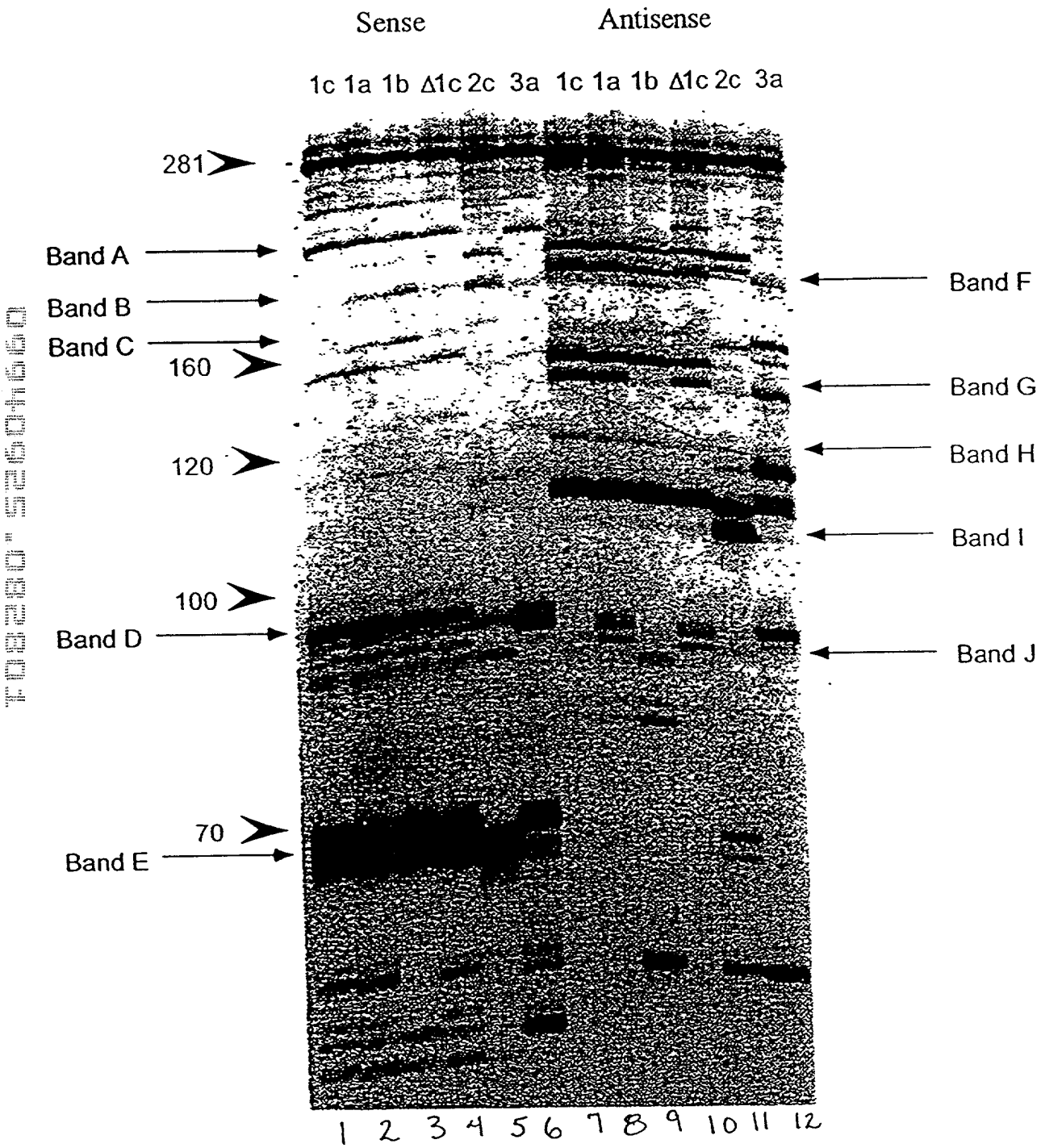




FIGURE 84

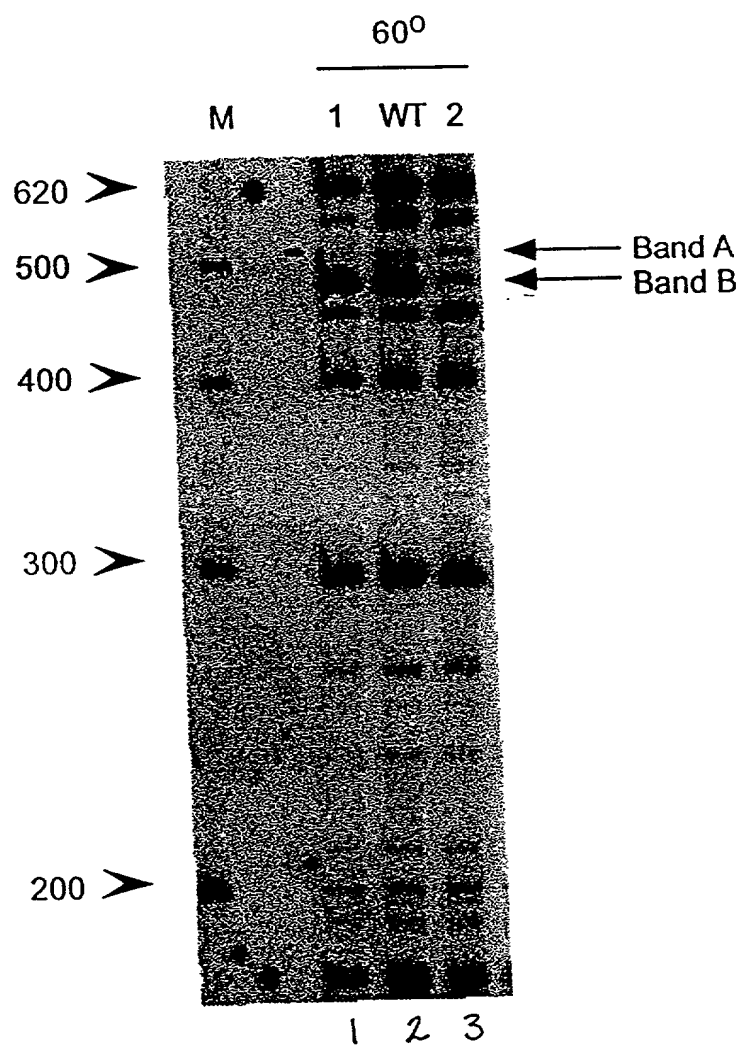
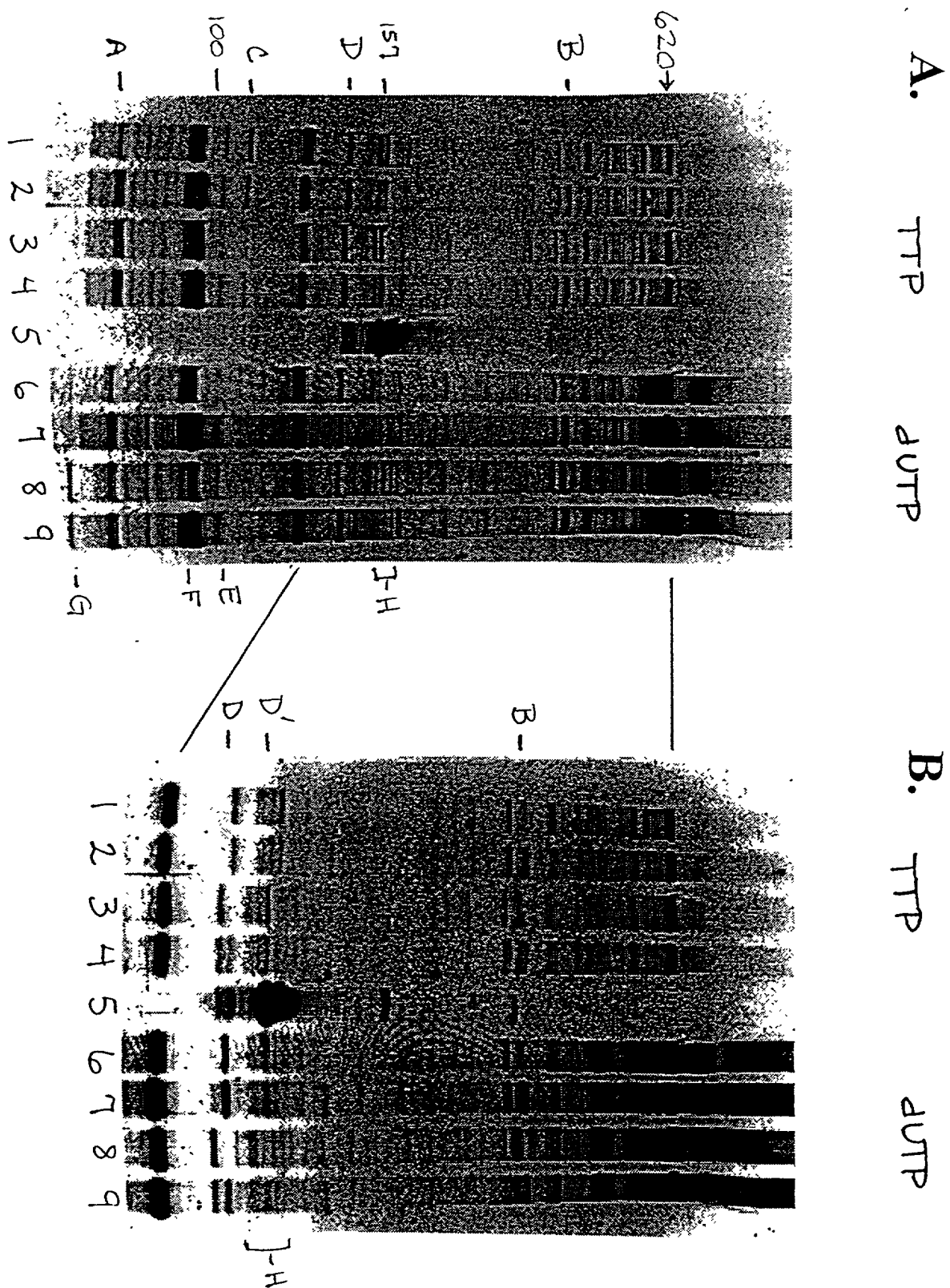


FIGURE 85



09940925.082801

FIGURE 86

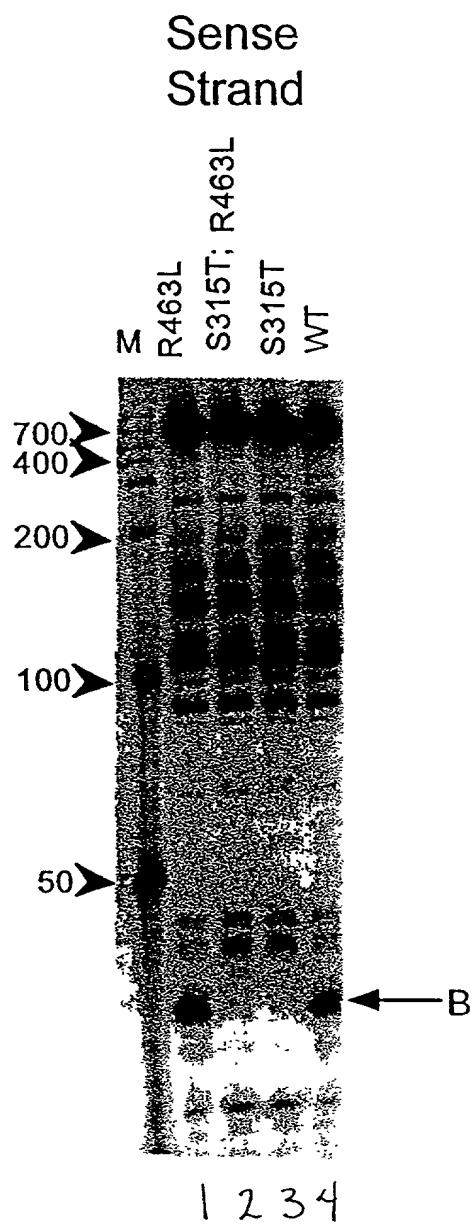
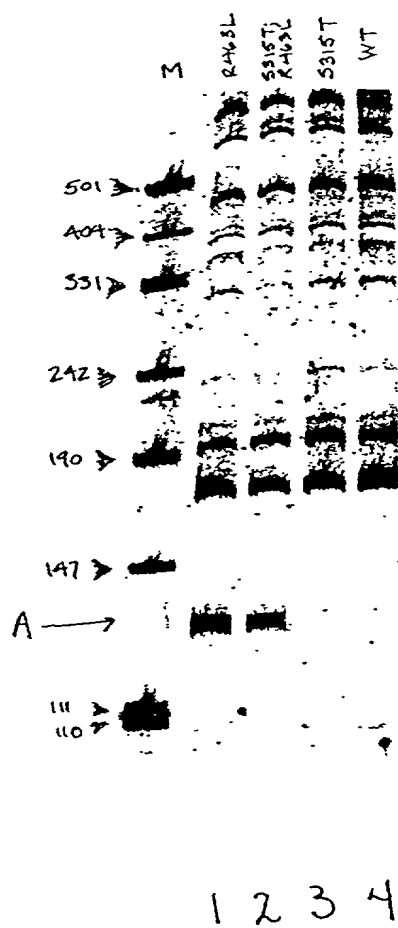


FIGURE 87

Antisense  
Strand



## FIGURE 88

Sheet 1/2

10 20 30 40 50 60 1638  
**AGA GTTTGATCCT GGCTCAG**  
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA  
TTTAACTTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

70 80 90 100 110 120 ER10  
**GGCGGAC GGGTGAGTAA**  
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA  
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCAT

130 140 150 160 170 180  
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT  
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA

190 200 210 220 230 240  
**AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG**  
**TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGAGAAC GGTAGCCTAC ACGGGTCTAC**

250 260 270 280 290 300  
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA  
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT

310 320 330 340 350 360  
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG  
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCACC  
**TGA GGATGCCCTC CGTCGTC** 1659

370 380 390 400 410 420  
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT  
CCTTATAACG TGTTACCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCTTCCGGA

430 440 450 460 470 480  
TCGGGTGTGA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT  
AGCCCAACAT TTCATGAAAG TCGCCCCTCC TTCCCTCAT TCAATTATGG AAACGAGTAA

490 500 510 520 530 540  
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG  
CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC

550 560 570 580 590 600  
GGTGCAAGCG TTAATCGGAA TTACTGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA  
CCACGTTTCG AATTAGCCTT AATGACCCGC ATTTTCGCGTG CGTCCGCCAA ACAATTACGT

610 620 630 640 650 660  
GATGTGAAAT CCCCgggGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC  
CTACACTTTA GGGGCCCCGAG TTGGACCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG

670 680 690 700 710 720  
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC  
CATCTCCCCC CATCTTAAGG TCCACATCGC CACTTTACGC ATCTCTAGAC CTCCTTATGG

730 740 750 760 770 780  
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA  
CCACCGCTTC CGCCGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTTCG CACCCCTCGT

101

790 800 810 820 830 840  
 AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC  
 TTGTCCTAAT CTATGGGACC ATCAGGTGCG GCATTTGCTA CAGCTGAACC TCCAACACGG  
 850 860 870 880 890 900  
 CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA  
 GAACTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAGCTGG CGGACCCCTC ATGCCGGCGT  
 910 920 930 940 950 960  
 AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAAGC GGTGGAGCAT GTGGTTTAAAT  
 TCCAATTTTG AGTTTACTTA ACTGCCCCCG GGCGTGTTTCG CCACCTCGTA CACCAAATTA  
 970 980 990 1000 1010 1020  
 TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG  
 AGCTACGTTG CGCTTCTTGG AATGGACCAG AACTGTAGGT GCCTTCAAAA GTCTCTACTC  
 1030 1040 1050 1060 1070 1080  
 AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA  
 TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAACACT  
 1090 1100 1110 1120 1130 1140  
 AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCC TTTGTTGCCA GCGGTCCGGC  
 TTACAACCCA ATTCAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCCG  
 1150 1160 1170 1180 1190 1200  
 ATG ACGTCAAGTC  
 ATG ACGTCAAGTC  
 CGGGAACCTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC  
 GCCCTTGAGT TTCCTCTGAC GGTCACTATT TGACCTCCTT CCACCCCTAC TGCAGTTCAG  
 1210 1220 1230 1240 1250 1260  
 ATCATGGCCC TTA  
 ATCATGGCCC TTACGA  
 ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG  
 TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCGC  
 1270 1280 1290 1300 1310 1320  
 ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAAC  
 TGGAGCGCTC TCGTTCGCCT GGAGTATTTT ACGCAGCATC AGGCCTAACC TCAGACGTTG  
 1330 1340 1350 1360 1370 1380  
 TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT  
 AGCTGAGGTA CTTACGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC CACTTATGCA  
 GC CACTTATGCA  
 1390 1400 1410 1420 1430 1440  
 TCCCGGGCCT TGTACACACC GCGGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT  
 AGGGCCCGGA ACATGTGTGG CGGGCAGTGT GGTACCCCTCA CCCAACGTTT TCTTCATCCA  
 AGGGCCCGGA ACATG  
 1450 1460 1470 1480 1490 1500  
 AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA  
 TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTACAGCATT  
 1510 1520 1530 1540 1550  
 CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA.....  
 GTTCCATTGG CATCCCTTG GACGCCAACC TAGTGGAGGA AT.....

SB-1

SB-3  
SB-4SB-3  
SB-4

1743

1743

Accession	Seq ID	Seq ID No	Seq
1638	(SEQ ID NO:151)	151	AGAGTTTGATCCTGGCTCAG
E.colirrsE	(SEQ ID NO:158) 0	158	...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5	(SEQ ID NO:159) 0	159	~TTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGTGCCCTAATACATGCA
Stp.aureus	(SEQ ID NO:160) 0	160	..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCCTAATACATGCA
ER10	(SEQ ID NO:152)	152	GGCGGACCGGG
E.colirrsE	(SEQ ID NO:158) 0	158	AGTCGAACCGTTAACAG_---GAAGAAGCTTGCTTCTTT_---GCTACGAGTGGCGGACCGGG
Cam.jejun5	(SEQ ID NO:159) 0	159	62 AGTCGAACGAT_---GAAGCTTCTAGCTTGCTAGAGTGA_---TTAGTGGCGCACCGGG
Stp.aureus	(SEQ ID NO:160) 0	160	61 AGTCGAGCGAA_---CGGACGAGAAGCTTGCTTCTCTGATG_---TT-AGCGGCGGACCGGG
ER10	(SEQ ID NO:152)	152	TGAGTAA
E.colirrsE	(SEQ ID NO:158) 0	158	114 TGAGTAATGTCTGGGA_--AAGTGCCTGATGGAGGGGGATAACTACTGGAACGGTAGCTAATA
Cam.jejun5	(SEQ ID NO:159) 0	159	114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAAACAGTTGGAACGACTGCTAATA
Stp.aureus	(SEQ ID NO:160) 0	160	113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTTCGGGAAACCGGAGCTAATA
E.colirrsE	(SEQ ID NO:158) 0	158	175 CCGCATAAAC_---GTGCAAGAC_---CAAAGAGGGGACCTTCG_--GGCCTCTTG
Cam.jejun5	(SEQ ID NO:159) 0	159	176 CTCATACTCTCTGCTTAAACACAAGTTGAGTAGG_GAAAG_---TTTT_---GCTGTCA
Stp.aureus	(SEQ ID NO:160) 0	160	175 CCGGATAATATTTGAACCGCATGGTTCAAAAGTGAAGACGGT_---CTT_---GCTGTCA
E.colirrsE	(SEQ ID NO:158) 0	158	221 CCATCGGATGTCCAGATGGGATTAGCTAGTGGGTAACGGCTCACCTAGGCGACGA
Cam.jejun5	(SEQ ID NO:159) 0	159	221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGTAATGGCTTACCAAGGCTATGA
Stp.aureus	(SEQ ID NO:160) 0	160	229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGTAACGGCTTACCAAGGCAACGA
E.colirrsE	(SEQ ID NO:158) 0	158	283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
Cam.jejun5	(SEQ ID NO:159) 0	159	283 CGCTTAACTGGTCTGAGAGGATGATCAGTCACTGGAACTGAGACACGGTCCAGACTCCTA
Stp.aureus	(SEQ ID NO:160) 0	160	291 TACGTAGCCGACCTGAGAGGGTGTATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
1659 (COMPL)			ACTCCTA
E.colirrsE	(SEQ ID NO:158) 0	158	345 CGGGAGGCAGCAGTGGGAAATATTGCACAATGGCGCAAGCCTGATGACGCCATGCCCGGTG
Cam.jejun5	(SEQ ID NO:159) 0	159	345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAAACCCCTGACGCAACGCCCGGTG
Stp.aureus	(SEQ ID NO:160) 0	160	353 CGGGAGGCAGCAGTAGGGAATCTTCCGAATGGCGGAAAGCCCTGACGGAGCAACGCCCGGTG
1659 (COMPL)			CGGGAGGCAGCAG
E.colirrsE	(SEQ ID NO:158) 0	158	407 TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGAGGAA_--GGGAGTAAAGTTAAT
Cam.jejun5	(SEQ ID NO:159) 0	159	407 GAGGATGACACTTTTCGGAGCGTAAACTCTCTTTTCTTAGGGAAG_---AATT_---AATT
Stp.aureus	(SEQ ID NO:160) 0	160	415 AGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAAAGTAA
E.colirrsE	(SEQ ID NO:158) 0	158	468 ACCTTTGCTCATTGACGTTTACCCGCGAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	(SEQ ID NO:159) 0	159	455 C_---TGACGGTACCTAAGGAATAAGCACCGGTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	(SEQ ID NO:160) 0	160	476 _TGTCACATCTTGACGGTACCTAATCAGAAAGCCACCGGCTAACTACGTGCCAGCAGCCGCG

*E. coli*rrsE 530 GTAATACGAGGGTGCAGCGTTTAACTGGGCGTAAAGCGCACGCGCGGTTT  
*Cam. jej*un5 506 GTAATACGAGGGTGCAGCGTTTAACTGGGCGTAAAGCGCGGTAGCGGATT  
*Stp. aure*us 538 GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGGTAGCGGTTT

*E. coli*rrsE 592 GTTAAGTCAGATGTGAAAATCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT  
*Cam. jej*un5 568 ATCAAGTCTCTTGTGAAAATCTAATGGCTTAACCATTAACCTGCTGGGAACTGATAGTCTA  
*Stp. aure*us 600 TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGTCATTGGAAAACCTGGAACCTT

*E. coli*rrsE 654 GAGTCTCGTAGAGGGGGTAGAATTCAGGTGTAGCGGTGAAATGCCGTAGAGATCTGGAGGA  
*Cam. jej*un5 630 GAGTGAGGGAGAGGCAGATGGAATTTGGTGTAGGGGTAAAATCCGTAGATATCAACCAAGA  
*Stp. aure*us 662 GAGTGCAGAAAGAGGAAAGTGAATTCATGTGTAGCGGTGAAATGCCGAGAGATATGGAGGA

*E. coli*rrsE 716 ATACCGGTGGCGAAGGCGGGCCCCCTGGACGAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA  
*Cam. jej*un5 692 ATACCCATTGCGAAGGCGATCTGCTGGAACCTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA  
*Stp. aure*us 724 ACACCAAGTGGCGAAGGCGACTTCTGGTCTGTAACCTGACGCTGATGTGCGAAAGCGTGGGGA

*E. coli*rrsE 778 GCAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC  
*Cam. jej*un5 754 GCAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGATACACTAGTTGTGGGT  
*Stp. aure*us 786 TCAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGATGCTAAGTGTTAGGGG

*E. coli*rrsE 840 C-CTTGA-GGCGTGGCTTCGGAGCTAACGCGTTAAGTCGACCCGCTGGGAGTACGGCCGC  
*Cam. jej*un5 816 G-CTAGT-CATCTCAGTAATGACGCTAACGCTTAAGTGTACCGCTGGGAGTACGGTCGC  
*Stp. aure*us 848 GT-TTCCGCCCTTAGTGCTGACGCTAACGCTTAAGCTCCGCTGGGAGTACGACCGC

*E. coli*rrsE 900 AAGGTTAAAACTCAAATGAATTGACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAAAT  
*Cam. jej*un5 876 AAGATTAAAACTCAAAGGAATAGACGGGGACCCGACAAAGCGGTGGAGCATGTGGTTTAAAT  
*Stp. aure*us 909 AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTTAAAT

*E. coli*rrsE 962 CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAT  
*Cam. jej*un5 938 CGAAGATACGCGAAGAACCTTACCTGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG  
*Stp. aure*us 971 CGAAGCAACGCGAAGAACCTTACCAAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC

*E. coli*rrsE 1024 GTG--CCTTCGGG--AA-CGGTGAGACAGGTGCTGCATGGCTGTCAGCTCGTGTGTGTGA  
*Cam. jej*un5 1000 GTGCTAGCTTGCTAGAA--CTTAGAGACAGGTGCTGCACGGCTGTCAGCTCGTGTGTGTGA  
*Stp. aure*us 1033 TTCC-CCTTCGGG--GGACAAAGTGACAGGTGCTGCATGGTTGTCAGCTCGTGTGTGA

SB-1  
*E. coli*rrsE 1081 AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTTGTGTCAGCGGTCCGG-CC  
*Cam. jej*un5 1061 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTAGTTGCTAACGTTCCGG-CC  
*Stp. aure*us 1092 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAAGCTTAGTTGCCATCA-TTAAGT-T



SB-3 (SEQ ID NO:157) ATGACGTCAAGTCATC  
SB-4 (SEQ ID NO:154) ATGACGTCAAGTCATC  
E.coli rse 1142 GGGAAGCTCAAGGAGACTGCCAGTGTAAACTGGAGGAAGGTGGGATGACGTCAAGTCATC  
Cam.jejun5 1122 GAGCACTCTAAATAGACTGCGCTTCG-TAAGGAGGAGGAAGGTGGACGATCAAGTCATC  
Stp.aureus 1152 GGGCACTCTAAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAAATCATC

SB-3 ATGGCCCTTA  
SB-4 ATGGCCCTTACGA  
E.coli rse 1204 ATGGCCCTTACGACCGGCTTACACACGTGCTACAAATGGCGCATACAAAGAGAGCCTC  
Cam.jejun5 1183 ATGGCCCTTATGCCAGGGCGACACACGTGCTACAAATGGCATATAGATGACGCAATACC  
Stp.aureus 1214 ATGCCCTTATGATTTGGGCTACACACGTGCTACAAATGACAAATACAAAGGCGAAGAAC

E.coli rse 1266 GCGAGAGCAAGCGGACCTCATAAAGTGCCTGCTAGTCCGGATTGGAGTCTGCACTCGACTC  
Cam.jejun5 1245 GCGAGGTGGAG-CAATCTATAAATATGTCCAGTTCCGATTGTTCTCTGCACTCGAGAG  
Stp.aureus 1276 GCGAGGTCAAGCAAAATCCCATAAAGTTGTTCTCAAGTTGGATTGTAGTCTGCACTCGACTA

E.coli rse 1328 CATGAAGTCGGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC  
Cam.jejun5 1306 CATGAAGCCGGAAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT  
Stp.aureus 1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT  
1743 (comp1) CGGTGAATACGTTCCCGGGC

E.coli rse 1389 CTTGTACACACCGCCCGTCAACCATGGGAGTGGGTGCAAAAGAGTAGGTAAGCTTAACCT  
Cam.jejun5 1368 CTTGTACTCACCGCCCGTCAACCATGGGAGTGAATTCATCTGAAAGCCGGAATACT-A-A  
Stp.aureus 1399 ATTGTACACACCGCCCGTCAACCATGGGAGTGTGTAACCCGAAGCCGGTGGAGTAACCT  
1743 (comp1) CTTGTAC

E.coli rse 1451 TCG-GGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAGTGCATAACAAGTAAACG  
Cam.jejun5 1427 AC--T-AGTTACCGTCCACAGTGAATCAGCGACTGGGGTGAGTGCATAACAAGTAAACG  
Stp.aureus 1461 TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAGTGCATAACAAGTAAACG

E.coli rse 1512 TAGGGGAACCTGCGGTTGGATCACTCCTTA---  
Cam.jejun5 1485 TAGGAGAACTGCGGTTGGATCACTCCT---  
Stp.aureus 1523 TATCGGAAGGTGCGGCTGGATCACTCCTTTCT-

FIGURE 90

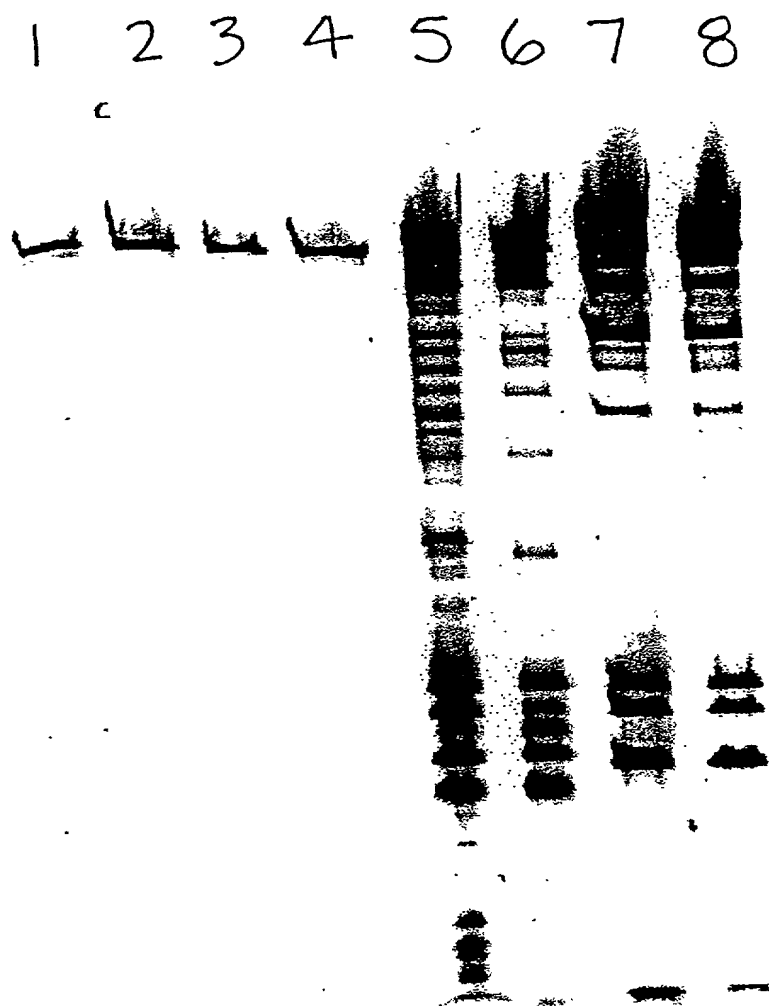
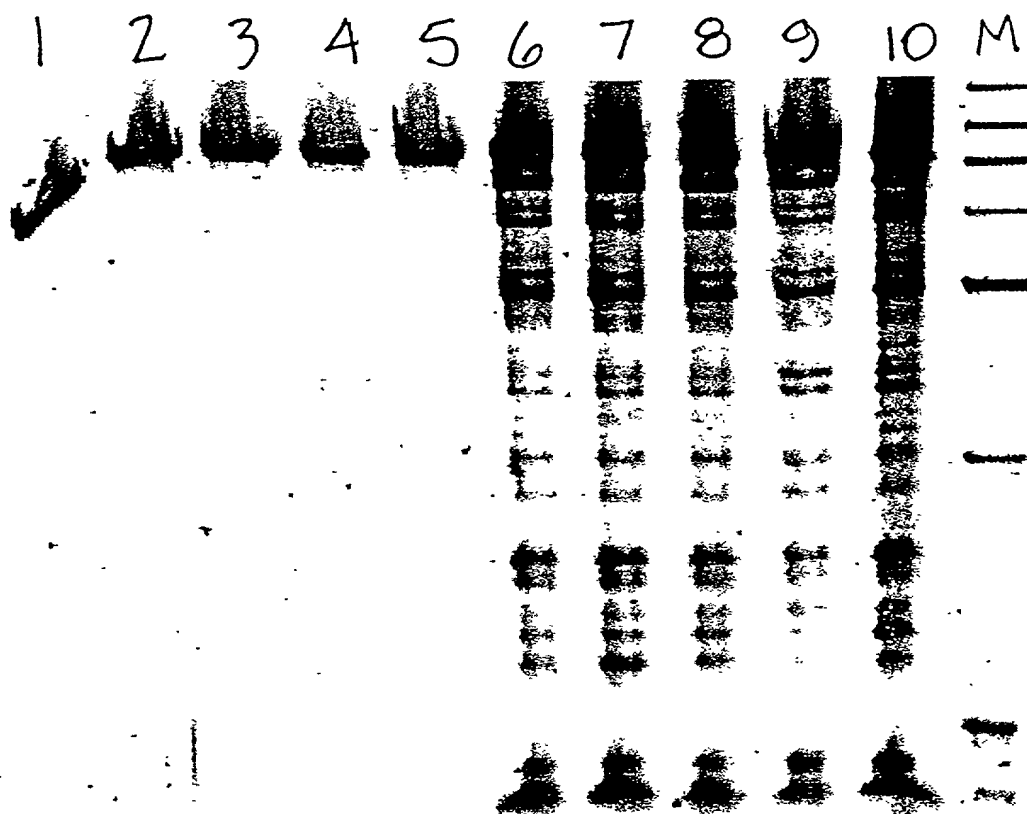


FIGURE 91

A.



B.

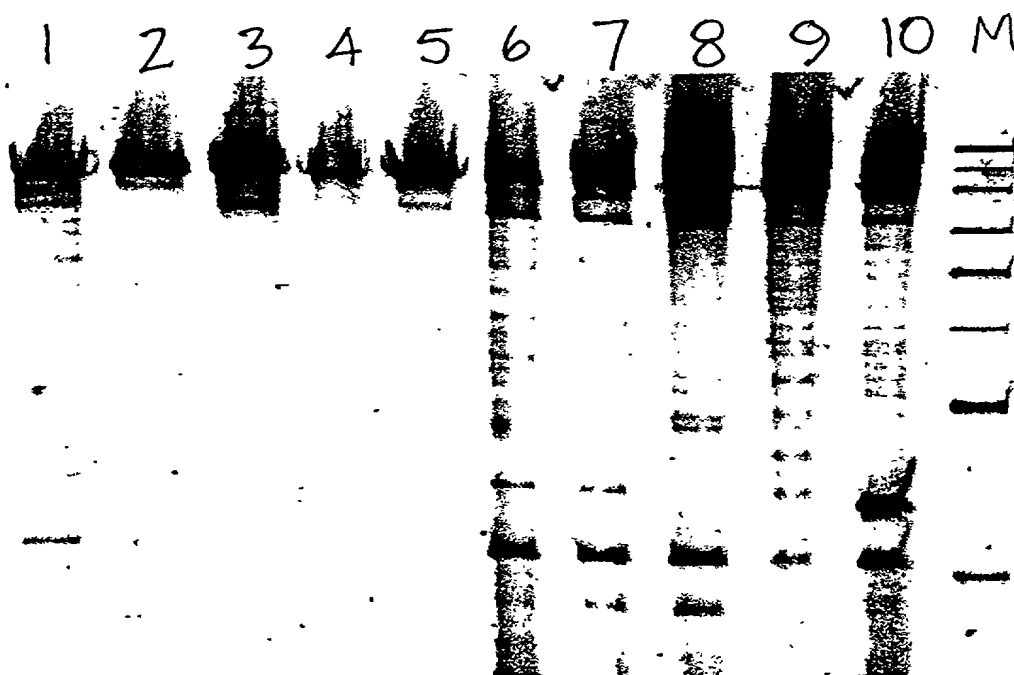


FIGURE 92

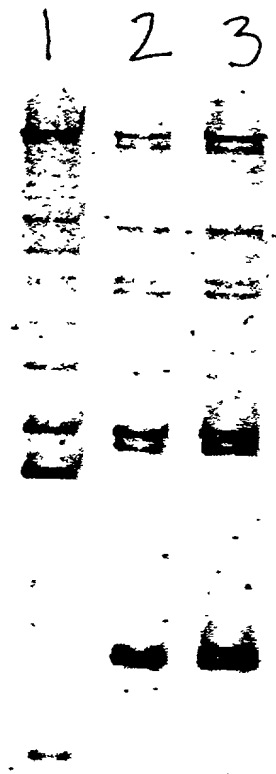
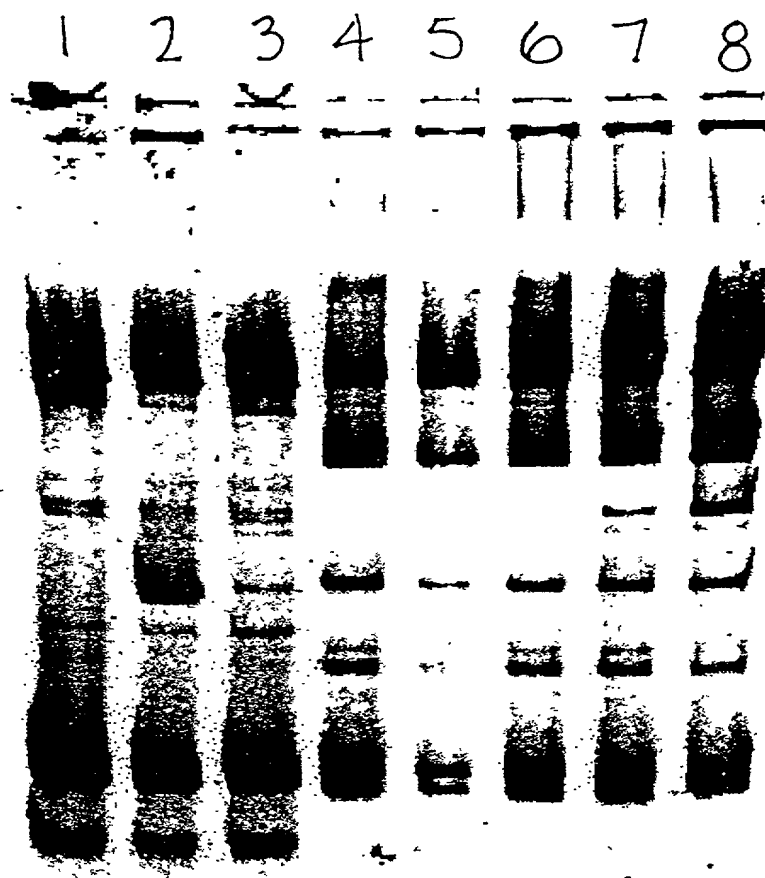


FIGURE 93



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FIGURE 94

